

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-383 <STO>
A:Cross-references: UNIPROT:Q9SYH3; GB:AR005173; NID:94587558; PIDN:AAD25789.1; GSPDB:GN
C:Genetics:
A:Gene: FLS11.25
A:Map position: 1

Query Match 11.0%; Score 201; DB 2; Length 383;
Best Local Similarity 21.5%; Pred. No. 1.5e-07;
Matches 81; Conservative 71; Mismatches 171; Indels 54; Gaps 13;

Qy 14 LLGTTSVTAALYSV-YRQARVSQELKGAKKVHLGDLKLSILSEAPGKVP-----64
Db 23 ILGTLAVSAVGSALKYASTNAALKTKDAPEVSI-SDLRSLPASEDKSETNDRKSN81
Qy 65 --YAVIEGAVRSVETLNSQVENCCKGVIQRLTLQEHKVMWNRTHLWNCDSKIIHOR--120
Db 82 QRIVVVRGVK--PKISDEGKNNVLLSPETGDKALIORTQTVYVSGMKRLFPQSTGH139
Qy 121 -----TNTVPFDLPVHEDGVD---VAVRV---LKPDLSDVLGLETVEYKFP159
Db 140 RFMLERSLRKHGADFTRTVPFVGVKQSQNSSFVAVNMGSRQPLP-----LTTVYNRL194
Qy 160 HPSIQSFDTVICHVISGRPKGIQETHEMLKVGATLTCVGLVDNNSVRLQPPKQGMQY219
Db 195 QPINSSFLQA---FLYPDYPVGLLDIEKILPGDKDITAVG-IYFNNVGPEIKSCQDLFPY250
Qy 220 YLSSQDFDLQROESSVRLMKVALVFGFATCATLFFILRKQYLQORERLRLKOMOEFP279
Db 251 FLSEMTDKMIEDLMEQTNFIFLGSVILGIVSGILSYAAVRTW---NKKWQMNHOREL306
Qy 280 QEHEAQLLSRAKPEDRESLSKA--CVVCLSSFKSCVFLGCHVCSCTCYRALPEP--KK335
Db 307 PORPNDSVVDDEPEDAEIPDGELCVICVSRRRVPAPFCGHVWCRCRCASTVERELNPK366
Qy 336 CPICRQAITRVIPLNS 352
Db 367 CPVCLQSIGRSMRVYS 383

RESULT 3
B96664
probable RING zinc finger protein T12P18.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96664
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <STO>

A:Cross-references: UNIPROT:Q9CAK3; GB:AE005173; NID:g6358794; PIDN:AAF07375.1; GSPDB:GN
C:Genetics:
A:Gene: T12P18.8
A:Map position: 1

Query Match 7.6%; Score 138.5; DB 2; Length 115;
Best Local Similarity 30.2%; Pred. No. 0.0016;
Matches 35; Conservative 19; Mismatches 46; Indels 17; Gaps 4;

Qy 248 GFATCATLFFILR---KQYLQORERLRLKOMOEFGHEAQLLSRAKPEDRESLSKA---301
Db 2 GF-TVLGVFLITKHVIDSVLERRRRLQKRVLDAAAKRAELESESGNSGTSIDSTKK60
Qy 302 -----CVVCLSSFKSCVFLGCHVCSCTCYRALPEPKKPCICRQAITRVIPLY350
Db 61 EDVAPDLCVLCLEQYNAVFPVCGHMCCTACSSHL---TSCPLCRRRIDLAVKTY113

RESULT 4
S68450
apoptosis inhibitor hiap-2 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68450
R:Liston, P.; Roy, N.; Tamai, K.; Lefebvre, C.; Baird, S.; Cherton-Horvat, G.; Farahani
Nature 379, 349-353, 1996
A:Title: Suppression of apoptosis in mammalian cells by NAIP and a related family of IA
A:Reference number: A58182; MUID:96149249; PMID:8552191
A:Accession: S68450
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-618 <L1S>
A:Cross-references: UNIPROT:Q13490; EMBL:U45879; NID:gl184317; PIDN:AAC50372.1; PID:gl1
C:Function:
A:Description: apoptotic suppressor
C:Keywords: apoptosis; zinc finger
P:567-611/Domain: RING finger homology <RNG>

Query Match 7.6%; Score 138.5; DB 2; Length 618;
Best Local Similarity 21.5%; Pred. No. 0.014;
Matches 67; Conservative 50; Mismatches 119; Indels 75; Gaps 13;

Qy 82 QFVENCCKGVIQRLTLQEHKVMWNRTHLWNCDSKIIHRTNTPFDLPVHEDGVDAVVR141
Db 343 EFVDEIQRYPHLL--EQLLSTDDTGTENADPPIIH-----FGGSSSSSDAVMM391
Qy 142 LKPL--DSVDLGL-----ETVYKFPHSIQSF---TDVIGHYISGERPKIQE---TE186
Db 392 NTPVVKSALEMGFNRLVKQTVLSKILTGTENYKTVNDIVSALLNAEDEKREKQAE451
Qy 187 EMLKVGATLTGVGL-----VLDN-----NSVRLQPP---KQGMQYVLSQD-FD227
Db 452 EMASDDLIRKRNWALFQQLTCVLPILDNLKANVINKQEHDDIHKQTIQIPLOARELID511
Qy 228 SLLQROESSVRLMKVALVFGFATCATLFFILRKQYLQOE-----RLRLKOMOEFOE281
Db 512 TIWKGNAANIFKNKLEIDSTLYKNLFVDKMKVYIPTEVDVSLGSLERLQOE---568
Qy 282 HEAQLLSRAKPEDRESLSKACVCLSSFKSCVFLGCHVCSCTCYRALPEPKKPCICRQ341
Db 569 -----RTCKVCMDKEVSVVVFPCGHLWVQEC---APSLURKPCICRG607
Qy 342 AITRVIPLNS 352
Db 608 IIKGTVRIFLS 618

RESULT 5
S68449
apoptosis inhibitor hiap-1 - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: S68449

RESULT 10
A96664

unknown protein t12p18.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A96664
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; E.
ansen, N.F.; Hughes, B.; Huizar, L.
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:210167519; PMID:11130712

A:Molecule type: DNA
A:Residues: 1-200 <STO>
A:Cross-references: UNIPROT_Q9CAK2; GB:AE005173; NID:G6358784; PIDN:AAF07365.1
C:Genetics:
A:Gene: Tl2p18.9
A:Map position: 1

	Query Match	Score 6.8†	Score 124.5;	DB 2;	Length 200;
	Best Local Similarity	28.0‡	Pred. No. 0.036;		
	Matches 52;	Conservative 31;	Mismatches 94;	Indels	Gaps
Qy	17	TTSVVTAALYSVYRQKARVSQELKGAKKVHGLDLSILSEAPGKCVPYAV-IEGA	VRSV	75	
		: : : : : :	: : : : :		
Dd	8	TCCLSAALYLGRSSGDRAEVLVTVRVNQLKELAQLL-EUDSKILPIVAVSGRVGS-	65		
		: : : : : :	: : : : :		
Qy	76	KETINSQFVENCKGVIQELTLQHKVMWNRTHLNDCSKIHQRTNTVPFDLPHPEDGV	135		
		: : : : : :	: : : : :		
Dd	66	-ETPIKEHSIRGVIVVEETAQHFLKKNETGS-WWDQSALMLMSKSKEVPWF--DDGT	120		
		: : : : : :	: : : : :		
Qy	136	DVAVRVLKPDSVDLGLETVYEKPHPSIQSFDTDVIGHYISGBRPKGIOSTEEMLKVGATL	195		
		: : : : : :	: : : : :		

```

Db      121  S-RVHVMGARGATGATVGSEVPESGRSLVRGTLVDYLQGLKMLGVKRIERVLPTGIPL 179
Qy      196  TGVGEL 201
      |  |||:
Db      180  TIVGEV 185

RESULT 11
A45679
inhibitor-of-apoptosis polypeptide (IAP) - Cydia pomonella granulosis virus CpGV
C:Species: Cydia pomonella granulosis virus CpGV
C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: A45679
R:Crook, N.E.; Clem, R.J.; Miller, L.K.
J. Virol. 67, 2168-2174, 1993
A>Title: An apoptosis-inhibiting baculovirus gene with a zinc finger-like motif
A:Reference number: A45679; MOID:93188168; PMID:8445726
A:Accession: A45679
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <CRO>
A:Cross-references: UNIPROT:P41436; GB:I05494; NID:G289583; PIDN:AAA43835.1; E
A:Note: sequence extracted from NCBI backbone (NCBIN:127014, NCBIP:127015)
C:Superfamily: viral apoptosis inhibitor IAP; RING finger homology

Query Match      6.7%; Score 123; DB 2; Length 275;

```


Figure 1

A:Accession: T16028
A:Status: preliminary; translated from GB/EMBL/DBAJ

1. *Introduction*

A;Molecule type: DNA
A;Residues: 1-824 <TAI>
A;Cross-references: EMBL:U40945; NID:g1072208; PID:g1072213; PIDN:AAA81723.1; CESP:F10D7
C;Genetics:
A;Gene: CESP:F10D7.5
A;introns: 83/1; 108/1; 136/2; 174/1; 217/1; 236/2; 278/2; 325/3; 354/3; 384/1; 399/3; 4
C;Superfamily: fruit fly inger protein neuralized; RING finger homology
F;769-817/Domain: RING finger homology <RRN>

Query Match 6.4%; Score 117.5; DB 2; Length 824;
Best Local Similarity 34.7%; Pred. No. 0.77;
Matches 26; Conservative 7; Mismatches 35; Indels 7; Gaps 2;

Qy 279 FQHEAQLLSRAKPEDRESILKSAVCVCLSSFKSCVFLECGHVCSCTECYRALPEPK-KCP 337
Db 756 FQNEGNGAQEVNEGDE-----CTICMDAPVNSVLYTCGHMCMCFECGRLLTTKGTCP 809

Qy 338 ICRQAITRVIPLVNS 352
Db 810 ICRAPVDVITKYS 824

Search completed: November 6, 2004, 17:39:02
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 20:11:02 ; Search time 9629 Seconds
(without alignments)
11570.727 Million cell updates/sec

Title: US-09-978-360A-32
Perfect score: 2356
Sequence: 1 atccctggcgccacagtcgg.....aaccaaaaaaaaaaaaaa 2356

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2356	100.0	2356	6	AR306576
2	2356	100.0	2356	6	AX061650
3	2356	100.0	2374	9	BC014010
4	2345	99.5	2382	9	BC010101
5	2338.4	99.3	2413	6	AX191590
6	2336.8	99.2	2401	6	BD170650
7	2335.2	99.1	2401	6	BD170649
8	2335.2	99.1	2401	6	AB097015
9	2332	99.0	2442	6	AX879967
10	2332	99.0	2442	6	BD158122
11	2332	99.0	2442	9	AK022937
12	2330.8	98.9	2431	6	AX428888
13	2291.8	97.3	2717	6	AX405813
14	2217	94.1	2377	6	AX274867
C 15	1973.4	83.8	195076	9	AL391357
C 16	1951.4	82.8	126141	2	AL356300
C 17	1768.2	75.1	163801	2	AC025224
C 18	1059	44.9	1059	6	AX191580
C 19	862	36.6	972	6	CQ727201

20	846.6	35.9	1354	10	BC019516	BC019516 Mus muscu
21	589	25.0	259224	2	AC109006	AC109006 Rattus no
C 22	584.2	24.8	170878	2	AC107845	AC107845 Mus muscu
23	584.2	24.8	248479	10	AL807249	AL807249 Mouse DNA
24	479.6	20.4	1143	5	BC068869	BC068869 Xenopus 1
C 25	476.6	20.2	512	6	AX873089	AX873089 Sequence
C 26	476.6	20.2	512	6	BD153151	BD153151 Primer fo
C 27	363	15.4	374	6	AX333839	AX333839 Sequence
28	338.8	14.4	484	6	AX868018	AX868018 Sequence
29	338.8	14.4	484	6	BD148080	BD148080 Primer fo
30	309	13.1	343	6	BD077897	BD077897 5'EST of
31	307.4	13.0	378	6	BD076018	BD076018 5' EST of
32	304.6	12.9	391	6	BD076940	BD076940 5' EST of
33	298.2	12.7	184991	2	BX927120	BX927120 Danio rer
C 34	294.2	12.5	476	11	G26878	G26878 human STS S
35	200.6	8.5	201	11	BV199951	BV199951 sqm20280
36	195.2	8.3	260	6	CQ659938	CQ659938 Sequence
37	162.4	6.9	175	6	CQ657979	CQ657979 Sequence
C 38	146.6	6.2	162087	5	BX649599	BX649599 Zebrafish
39	142.2	6.0	2674	5	BC059797	BC059797 Danio rer
40	124.6	5.3	197	6	BD075982	BD075982 5' EST of
41	113.4	4.8	2748	5	BC079729	BC079729 Xenopus 1
42	95.6	4.1	1086	6	CQ572652	CQ572652 Sequence
43	95.6	4.1	1243	3	AX113263	AX113263 Drosophil
C 44	74.6	3.2	3475	6	CQ572651	CQ572651 Sequence
45	74.6	3.2	45258	2	AC015395	AC015395 Drosophil

ALIGNMENTS

RESULT 1	AR306576	2356 bp	DNA	linear	PAT 12-JUN-2003
LOCUS	Sequence 55 from patent US 6548633.				
DEFINITION	AR306576				
ACCESSION	AR306576.1				
VERSION	GI:31696645				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2356)				
AUTHORS	Edwards, J.-B. D.M., Bougueret, L. and Jobert, S.				
TITLE	Complementary DNA's encoding proteins with signal peptides				
JOURNAL	Patent: US 6548633-A 55 15-APR-2003;				
FEATURES	Location/Qualifiers				
source	1..2356				
	/organism="unknown"				
	/mol_type="genomic DNA"				

ORIGIN

Query Match	100.0%	Score 2356;	DB 6;	Length 2356;
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Matches 2356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	ATCCTTGGCGCCACAGTCGCGCCACCGGGCTCGCCGCGTCATGGAGAGCGGGGGCGG		60
Qy	61	CCTCGTGTGCCAGTTTCCTCTGGGACCACTCTGTGTGTACCGCGCCCTGTACT		120
Db	61	CCTCGTGTGCCAGTTTCCTCTGGGACCACTCTGTGTGTACCGCGCCCTGTACT		120
Qy	121	CCGTGTACCGGAGAGCGCGGGTCTCCCAAGAGCTCAAGGAGCTCAAAAAGTTCAAT		180
Db	121	CCGTGTACCGGAGAGCGCGGGTCTCCCAAGAGCTCAAGGAGCTCAAAAAGTTCAAT		180
Qy	181	TGGGTGAAGATTAAAGAGTATCTTTCAGAGCTCCAGGAAATCCGTCCTTATGCTG		240
Db	181	TGGGTGAAGATTAAAGAGTATCTTTCAGAGCTCCAGGAAATCCGTCCTTATGCTG		240
Qy	241	TTATAGAGGAGCTGTGGGTCTGTTAAAGAACGCTTAACAGCCAGTTTGGGAAACT		300

241	TTATAGAGGAGCTGTGGGTCTGTTTAAAGAACCGCTTAACAGCCAGTTTGTGGAAAACT	300	1381	ACTGAAATGCCTCATCTTAAGCACCAAGCCAGTGATCAGAGCTCTTCTGTTCCTG	1440
301	GCAGGGGTAATTCAGGGCTGACACTTCAGAGCACAGATGGTGGAAATCGAACCA	360	1381	ACTGAAATGCCTCATCTTAAGCACCAAGCCAGTGATCAGAGCTCTTCTGTTCCTG	1440
301	GCAGGGGTAATTCAGGGCTGACACTTCAGAGCACAGATGGTGGAAATCGAACCA	360	1441	TGCTCTCTGTTTTTTTCTGTGTAATCGTGTCTGTGTGGACTTGTGGAGGACTCAGAG	1500
361	CCACCTTTTGGATGATTGCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG	420	1441	TGCTCTCTGTTTTTTTCTGTGTAATCGTGTCTGTGTGGACTTGTGGAGGACTCAGAG	1500
361	CCACCTTTTGGATGATTGCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG	420	1501	GGAGGAAAGGCTGGGCCCCGAGTACAAACGATGCTTGGTGTCTGCTCCGAGAGACT	1560
421	ACCTGTGCCCCCAGAGATGGGTGATGTGGTGTGGAGTCTGAAAGCCCTGCACT	480	1501	GGAGGAAAGGCTGGGCCCCGAGTACAAACGATGCTTGGTGTCTGCTCCGAGAGACT	1560
421	ACCTGTGCCCCCAGAGATGGGTGATGTGGTGTGGAGTCTGAAAGCCCTGCACT	480	1561	CTGCCGAGCTTTCTTTCTTTTCTCATGCCCCCGGAAACAGTCTTTCTCAGAAATGT	1620
481	CAGTGGATCTGGTCTAGAGACTGTGTATGAAAGTTCCACCCCTCCGATTCAGTCTTCA	540	1561	CTGCCGAGCTTTCTTTCTTTTCTCATGCCCCCGGAAACAGTCTTTCTCAGAAATGT	1620
481	CAGTGGATCTGGTCTAGAGACTGTGTATGAAAGTTCCACCCCTCCGATTCAGTCTTCA	540	1621	CAGCTGGGAGGCTCAACTTGTCTTCTTCCCTCACCTTGCCTTCCCTTAACGCTG	1680
541	CCGATGTCATCGCCACTACATCAGCGTGAAGCGGCCCAAGGATCCAGAGACCGAGG	600	1621	CAGCTGGGAGGCTCAACTTGTCTTCTTCCCTCACCTTGCCTTCCCTTAACGCTG	1680
541	CCGATGTCATCGCCACTACATCAGCGTGAAGCGGCCCAAGGATCCAGAGACCGAGG	600	1681	CACGTGTGTAGAGGACAAAGAAAGTGAAGTCAAGACATCCGCTTCTGCCAGATGT	1740
601	AGATGCTGAAGTGGGGCCACCTTCACAGGGTTGGGAACTGGTCTTGACACAACT	660	1681	CACGTGTGTAGAGGACAAAGAAAGTGAAGTCAAGACATCCGCTTCTGCCAGATGT	1740
601	AGATGCTGAAGTGGGGCCACCTTCACAGGGTTGGGAACTGGTCTTGACACAACT	660	1741	CGGGCCCCGGGCAACAGTTGAAGAGATCATGTGAAGGCGAGTTGGTCAGGAGGCC	1800
661	CTGTCGGCTGAGCGGCCCAACAGGATGCACTATCTAAGCAGCCAGGACTTTCG	720	1741	CGGGCCCCGGGCAACAGTTGAAGAGATCATGTGAAGGCGAGTTGGTCAGGAGGCC	1800
661	CTGTCGGCTGAGCGGCCCAACAGGATGCACTATCTAAGCAGCCAGGACTTTCG	720	1801	TCCTGGTTTCGCCACTGGCCCTCTGAAATTCCTCTGCCACTTGGAGAGCTCGGGGTGT	1860
721	ACAGCTCTGTCAGAGGAGGAGTCAAGCTCAGGCTCTGGAAGTGTGGCGCTGGTTT	780	1801	TCCTGGTTTCGCCACTGGCCCTCTGAAATTCCTCTGCCACTTGGAGAGCTCGGGGTGT	1860
721	ACAGCTCTGTCAGAGGAGGAGTCAAGCTCAGGCTCTGGAAGTGTGGCGCTGGTTT	780	1861	CCCTGGTTTCCTCTCGAGAGTCAAGGCGAGAGGCTCGGCTCTCTGAAGACGCACTG	1920
781	TTGGCTTTGCCACATGTGCCACCTCTTCAATTCCTCGGAAGAGTATCTGCAGCGC	840	1861	CCCTGGTTTCCTCTCGAGAGTCAAGGCGAGAGGCTCGGCTCTCTGAAGACGCACTG	1920
781	TTGGCTTTGCCACATGTGCCACCTCTTCAATTCCTCGGAAGAGTATCTGCAGCGC	840	1921	TGGATGCCACTGGCCCTAGTGTCTTGGCCCTCAAGGCTTCTTGAAGGCTGTCAAGGAA	1980
841	AGAGCGCTGGCCCTCAAGCAGATCAGGAGGAGTTCCAGAGCATGAGGCCAGCTGC	900	1921	TGGATGCCACTGGCCCTAGTGTCTTGGCCCTCAAGGCTTCTTGAAGGCTGTCAAGGAA	1980
841	AGAGCGCTGGCCCTCAAGCAGATCAGGAGGAGTTCCAGAGCATGAGGCCAGCTGC	900	1981	AAGCAGCGGCTGGCAACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCGCTG	2040
901	TGAGCGAGCAAGCTCTGAGCAGAGGAGTCTGAAGAGCGCTGTGTGTGTCTGA	960	1981	AAGCAGCGGCTGGCAACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCGCTG	2040
901	TGAGCGAGCAAGCTCTGAGCAGAGGAGTCTGAAGAGCGCTGTGTGTGTCTGA	960	2041	CAGCTTTGACATCTTGGTGTACTCATGTCTCTCTCTTGTGTACCCCTCCAGTATT	2100
961	GCAGCTTCAAGTCTCTGCTTCTGAGTGTGGGACGTTTCTTCTGACCGAGTCT	1020	2041	CAGCTTTGACATCTTGGTGTACTCATGTCTCTCTCTTGTGTACCCCTCCAGTATT	2100
961	GCAGCTTCAAGTCTCTGCTTCTGAGTGTGGGACGTTTCTTCTGACCGAGTCT	1020	2101	ACCATTTGCCCTCACTGCCCCCTTGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT	2160
1021	ACCGCGCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGGTGA	1080	2101	ACCATTTGCCCTCACTGCCCCCTTGGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT	2160
1021	ACCGCGCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGGTGA	1080	2161	TCGCCACCTCTGAGTAGTTGGAGTGCATACACAGCTCTTTTATTTGCTTTCT	2220
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LOCUS

2356 bp DNA linear PAT 24-JAN-2001

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REFERENCE
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0149728-A, 112 12-JUL-2001;
 Protegene Inc. (JP); SAGAMI CHEMICAL RESEARCH CENTER (JP)
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BD170650
LOCUS
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REFERENCE
AUTHORS
TITLE
JOURNAL

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PN WO 02053737-A/38
PD 11-JUL-2002
PF 25-DEC-2001 WO 2001JP011389
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primers for synthesising full-length cDNA and their use
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Research Association for Biotechnology (JP)
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2335; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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BD158122			
LOCUS			

RESULT 10
 BD158122 2442 bp DNA linear PAT 17-JAN-2003
 LOCUS
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 DEFINITION
 ACCESSION BD158122
 VERSION BD158122.1 GI:27863880
 KEYWORDS JP 2002191363-A/12965.
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2442)
 Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto.J.,
 Teibi.S., Suciivama.T., Wakamatsu.A., Nagai.K. and Otsuki.T.

TITLE	Primer for synthesizing full-length cDNA and use thereof
JOURNAL	Patent: JP 2002191363-A 12965 09-JUL-2002;
COMMENT	HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/12965 PD 09-JUL-2002 PF 28-JUL-2000 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO, PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT CDS (144)..(1199).
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Best Local Similarity	99.8%; Pred. No. 0;
Matches 2335; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Sato, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Murakawa, K., Yamazaki, M., Ishibashi, T., Yamashita, H., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hoota, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsuura, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satch, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukumizu, Y., Fujimori, Y., Komiyama, M., Kuroki, T., Taniguchi, T., Endiwara, T., Ono, T., Yamada, K., Fujii, Y.,					

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 REFERENCE
 1 Hillman, J.L., Baughn, M.R., Yue, H., Lal, P., Lu, D.A., Patterson, C.,
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1 (bases 1 to 195076)
Kimberley, A.
Direct Submission
Submitted (25-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Oct 26, 2001 this sequence version replaced gi:16304938.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/RGP/Chr1
RP11-401M16 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.choi.org/bacpac/home.htm
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This sequence is the entire insert of clone RP11-401M16 The true
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true right end of clone RP4-749H3 is at 12964 in this sequence.

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Matches 1974; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 21969 GGCAGTCAACTGTGTCTCTTCCCTCACCTGTGCTTAAACGCTGCACGTGT 21910
Db |||||
QY 1688 GTGTAGAGACAAAGAAAGTCAAGTCAAGCAGTCTTCTTCAAGATTTGTCAAGCTG 1747
Db |||||
QY 21909 GTGTAGAGACAAAGAAAGTCAAGTCAAGCAGTCTTCTTCAAGATTTGTCAAGCTG 21850
Db |||||
QY 1748 CCGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGTGAGGCGAGTTGTGAGGCGCTCTCTGT 1807
Db |||||
QY 21849 CCGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGTGAGGCGAGTTGTGAGGCGCTCTCTGT 21790
Db |||||
QY 1808 TTCCGCACTGGCCCTGATTGAACTCTGCCACTTTGGGAGAGCTCGGGGTGTCTCCCTGT 1867
Db |||||
QY 21789 TTCCGCACTGGCCCTGATTGAACTCTGCCACTTTGGGAGAGCTCGGGGTGTCTCCCTGT 21730
Db |||||
QY 1868 TTCCCTCTCTGAGAAAGGCGAGAGGCTCTGCTCTCTGAGGACCGAGTGTGGATGC 1927
Db |||||
QY 21729 TTTCTCTCTGGAGATGAGGCGAGAGGCTCTGCTCTCTGAGGACCGAGTGTGGATGC 21670
Db |||||
QY 1928 CACTGGCTAGTGTCTGCTGCTCTCACAGCTTCTTGAAGGCTGTCAAGGAAAGCAGC 1987
Db |||||
QY 21669 CACTGGCTAGTGTCTGCTGCTCTCACAGCTTCTTGAAGGCTGTCAAGGAAAGCAGC 21610
Db |||||
QY 1988 CGGCTGGCACCTGAGCATATGCCCTCTTGGGGTCTCCCTCATCCAGCCCGTCGCAGCTTT 2047
Db |||||
QY 21609 CGGCTGGCACCTGAGCATATGCCCTCTTGGGGTCTCCCTCATCCAGCCCGTCGCAGCTTT 21550
Db |||||
QY 2048 GACATCTTGTGTACTCATGTGCTCTCTCTTGTGTTACCCCTCCAGTATTACCAATTT 2107
Db |||||
QY 21549 GACATCTTGTGTACTCATGTGCTCTCTCTTGTGTTACCCCTCCAGTATTACCAATTT 21490
Db |||||
QY 2108 GCGCCTCACCTGCTCTTGTGTGAGCTTTTGTGCAAGACAGATGGGCTGTTTCCGCCA 2167
Db |||||
QY 21489 GCGCCTCACCTGCTCTTGTGTGAGCTTTTGTGCAAGACAGATGGGCTGTTTCCGCCA 21430
Db |||||
QY 2168 CCTCTGAGTAGTGGAGGTACATACACAGCTCTTTTTTTATTTGCTCTCTGCTCTG 2227
Db |||||
QY 21429 CCTCTGAGTAGTGGAGGTACATACACAGCTCTTTTTTTATTTGCTCTCTGCTCTG 21370
Db |||||
QY 2228 AATGTTTCATCTCTGCTCTCTTGTGAGGCGAGGAGGCTGCTCTCAGGGGCCGACA 2287
Db |||||
QY 21369 AATGTTTCATCTCTGCTCTCTTGTGAGGCGAGGAGGCTGCTCTCAGGGGCCGACA 21310
Db |||||
QY 2288 CTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTGCAACCAA 2342
Db |||||
QY 21309 CTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTGCAACCAA 21255
Db |||||
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Qy	121	CCGTGTACCGCAGAGCCCGGGTCTCCCAAGAGCTCAAGCGAGCTAAAAAGTTCA	180
Db	121	CCGTGTACCGCAGAGCCCGGGTCTCCCAAGAGCTCAAGCGAGCTAAAAAGTTCA	180
Qy	181	TGGGTGAAGATTTAAAGAGTATCTTTTCAGAAGCTCCAGAAAAATCGTGCCTTATGCTG	240
Db	181	TGGGTGAAGATTTAAAGAGTATCTTTTCAGAAGCTCCAGAAAAATCGTGCCTTATGCTG	240
Qy	241	TTATAGAGGAGCTGTGCGGTCTGTTTAAAGAAACGCTTAACAGCCAGTTTGTGGAAACT	300
Db	241	TTATAGAGGAGCTGTGCGGTCTGTTTAAAGAAACGCTTAACAGCCAGTTTGTGGAAACT	300
Qy	301	GCAAGGGGGTAATTACAGCGCTGACACTTTCAGAGCACAAGATGCTGGAATCGAACC	360
Db	301	GCAAGGGGGTAATTACAGCGCTGACACTTTCAGAGCACAAGATGCTGGAATCGAACC	360
Qy	361	CCACCTTTGGGAATGATTCGCTCAAGATCATTCATCAGAGACCAACACAGTGCCTTTG	420
Db	361	CCACCTTTGGGAATGATTCGCTCAAGATCATTCATCAGAGACCAACACAGTGCCTTTG	420
Qy	421	ACCTGTTGCCCAAGAGATGGCGTGGATGTGCTGTGCAGTGTCTGAAGCCCTGACT	480
Db	421	ACCTGTTGCCCAAGAGATGGCGTGGATGTGCTGTGCAGTGTCTGAAGCCCTGACT	480
Qy	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCAGTCTTCA	540
Db	481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCAGTCTTCA	540
Qy	541	CCGATGTCATCGGCCACTATCATCAGCGGTGAGCGGCCCAAGGCGATCCAGAGACCGAGG	600
Db	541	CCGATGTCATCGGCCACTATCATCAGCGGTGAGCGGCCCAAGGCGATCCAGAGACCGAGG	600
Qy	601	AGATGCTGAAGGTGGGGGCCACCTCTCAGCGGTGGCGAACTGGTCTCGACACAACT	660
Db	601	AGATGCTGAAGGTGGGGGCCACCTCTCAGCGGTGGCGAACTGGTCTCGACACAACT	660
Qy	661	CTGTCCGCTGCAGCGGCCCAAAACAGGCATGCAGTACTATCTAAGCAGCCAGACTTCG	720
Db	661	CTGTCCGCTGCAGCGGCCCAAAACAGGCATGCAGTACTATCTAAGCAGCCAGACTTCG	720
Qy	721	ACAGCTGCTGCAGAGGCAGAGTGCAGCGTCTGGAAGTGTGCGCTGGTTT	780
Db	721	ACAGCTGCTGCAGAGGCAGAGTGCAGCGTCTGGAAGTGTGCGCTGGTTT	780
Qy	781	TTGGCTTTGCCACATGTGCCACCTCTTTCTTCAATCTCCGAAGCAGTATCTGCAGCGGC	840
Db	781	TTGGCTTTGCCACATGTGCCACCTCTTTCTTCAATCTCCGAAGCAGTATCTGCAGCGGC	840
Qy	841	AGGAGCGCTGCGCTCAGAGCAGATGCAGCGTCTGGAAGCAGTATCTGCAGCGGC	900
Db	841	AGGAGCGCTGCGCTCAGAGCAGATGCAGCGTCTGGAAGCAGTATCTGCAGCGGC	900
Qy	901	TGAGCCGAGCCAAAGCTCAGGACAGGAGTCTGAAGCGCTGTGTAGTGTGTCTGA	960
Db	901	TGAGCCGAGCCAAAGCTCAGGACAGGAGTCTGAAGCGCTGTGTAGTGTGTCTGA	960
Qy	961	GCAGCTTCAAGTCTGCGTCTTTCTGAGTGTGGCACGTTTCTCTGCA CGAGTGT	1020
Db	961	GCAGCTTCAAGTCTGCGTCTTTCTGAGTGTGGCACGTTTCTCTGCA CGAGTGT	1020
Qy	1021	ACCGGCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGTGA	1080
Db	1021	ACCGGCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGTGA	1080
Qy	1081	TACCCCTGTACAACTAATAGTTTGGAGCCGACAGCTTCACTTGAAGCACCCCTG	1140
Db	1081	TACCCCTGTACAACTAATAGTTTGGAGCCGACAGCTTCACTTGAAGCACCCCTG	1140
Qy	1141	CCCCCTTTTCAGGATTTTATCTCGAGGCTTTTGAGGACAGTGTGGGGTAGCTGT	1200
Db	1141	CCCCCTTTTCAGGATTTTATCTCGAGGCTTTTGAGGACAGTGTGGGGTAGCTGT	1200
Qy	1201	CACCTCCAGGTATGATTGAGGGAGGAATTTGGTAGAACTCTCCAGACCCATGCTCCAA	1260

1201	Db	CACCTCCAGGTATGATTCAGGGAGGAATTGGGTAGAACTCTCCAGACCCATGCCTCCAA	1260
1261	Qy	TGGCAGGATGCTGCCTTTCCACCTGAGAGGGGACCTGTCTCATGTGAGCCTCATCAGA	1320
1261	Db	TGGCAGGATGCTGCCTTTCCACCTGAGAGGGGACCTGTCTCATGTGAGCCTCATCAGA	1320
1321	Qy	GCCTCACCTCGGGAGATGCGGTGGGTCTCTCCAGGAGCAGATCAGTGCAGTGTG	1380
1321	Db	GCCTCACCTCGGGAGATGCGGTGGGTCTCTCCAGGAGCAGATCAGTGCAGTGTG	1380
1381	Qy	ACTGAAATGCCTCATCACTTAAGCAACAAAGCCAGTGATCAGCAGCTCTTTGTTCTGT	1440
1381	Db	ACTGAAATGCCTCATCACTTAAGCAACAAAGCCAGTGATCAGCAGCTCTTTGTTCTGT	1440
1441	Qy	TGTCCTCTGTTTTTTTCTGGTGAATCGTTGCTTGTGTGACATTGGTGAGGACTCAGAG	1500
1441	Db	TGTCCTCTGTTTTTTTCTGGTGAATCGTTGCTTGTGTGACATTGGTGAGGACTCAGAG	1500
1501	Qy	GGGAGAAAGGCTGGGCCCCGAGTACAACGGATGCCCTTGGGTGCTGCTCCGAAGAGACT	1560
1501	Db	GGGAGAAAGGCTGGGCCCCGAGTACAACGGATGCCCTTGGGTGCTGCTCCGAAGAGACT	1560
1561	Qy	CTGCCGACGTTTTCTTTCTTTTCTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1620
1561	Db	CTGCCGACGTTTTCTTTCTTTTCTCTCATGCCCCGGGAAACAGTCTTTCTTCAGAAATGT	1620
1621	Qy	CAGGCTGGGCAGGTCAACTGTGTGTTTCCCTCACTGCTTGCCTCTTAACGCGCTG	1680
1621	Db	CAGGCTGGGCAGGTCAACTGTGTGTTTCCCTCACTGCTTGCCTCTTAACGCGCTG	1680
1681	Qy	CAGTGTGTGTAGAGNCAAAAGAAAGTGAAGTCAGCACATCCGCTTCTGCCCAGATGGT	1740
1681	Db	CAGTGTGTGTAGAGNCAAAAGAAAGTGAAGTCAGCACATCCGCTTCTGCCCAGATGGT	1740
1741	Qy	CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTTGGTCAGGCAGGCC	1800
1741	Db	CGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTTGGTCAGGCAGGCC	1800
1801	Qy	TCCTGTGTTGCCACTGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGGGGTGGT	1860
1801	Db	TCCTGTGTTGCCACTGGCCCTGATTTGAACTCCTGCCACTTGGGAGAGCTCGGGGTGGT	1860
1861	Qy	CCCTGTGTTTCCCTCTGGAGAAAGAGCGCAGAGGCTCGCCTCTCAAGAGACGACGTG	1920
1861	Db	CCCTGTGTTTCCCTCTGGAGAAAGAGCGCAGAGGCTCGCCTCTCAAGAGACGACGTG	1920
1921	Qy	TGGATGCACCTGGCTAGTGTCTGGCCTCAAGCTTCTCTGCAAGGTGTCAACAAGAA	1980
1921	Db	TGGATGCACCTGGCTAGTGTCTGGCCTCAAGCTTCTCTGCAAGGTGTCAACAAGAA	1980
1981	Qy	AAGCAGCGGCTGGCACCTGAGCATATGCCCTCTTGGGGTCCCTCATCCAGCCCGTGG	2040
1981	Db	AAGCAGCGGCTGGCACCTGAGCATATGCCCTCTTGGGGTCCCTCATCCAGCCCGTGG	2040
2041	Qy	CAGCTTTGACATCTGTGGTACTCATGTGCTTCTCCTTGTGTATTACCCCTCCCACTAT	2100
2041	Db	CAGCTTTGACATCTGTGGTACTCATGTGCTTCTCCTTGTGTATTACCCCTCCCACTAT	2100
2101	Qy	ACCAATTTGCCCTCACTGCTGCCCTTGGTGAGCCTTTTGTGCAAGACAGATGGGGCTGTT	2160
2101	Db	ACCAATTTGCCCTCACTGCTGCCCTTGGTGAGCCTTTTGTGCAAGACAGATGGGGCTGTT	2160
2161	Qy	TCCCCCACTCTGAGTGTGAGGTCAATACAGAGCTCTTTTATTTATTTGCCCTTTTCT	2220
2161	Db	TCCCCCACTCTGAGTGTGAGGTCAATACAGAGCTCTTTTATTTATTTGCCCTTTTCT	2220
2221	Qy	GCCTCTGAATGTTTCACTCTGCTCCCTTGTGCAAGGCGAGGAGGGGTGCCCTCAGGG	2280
2221	Db	GCCTCTGAATGTTTCACTCTGCTCCCTTGTGCAAGGCGAGGAGGGGTGCCCTCAGGG	2280
2281	Qy	GCCGCACTAGTATGATGCACTGTGCAGTGTGAACAGCAGAAATTAACATGTTGCACCC	2340

Db	2281	GCACACTAGTATGATGCAGTGTCCAGTGTGAACAGAGAAATTAACAATGTTGCAACC	2340
QY	2341	AAAAAAAAAAAAAAAA	2356
Db	2341	AAAAAAAAAAAAAAAA	2356

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RESULT 2
US-08-905-223-188
; Sequence 188, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Ducloux, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: other
; LOCATION: 165..302
; IDENTIFICATION METHOD: blastn
; OTHER INFORMATION: identity 93
; OTHER INFORMATION: region 33..170
; OTHER INFORMATION: id T50032
; OTHER INFORMATION: est
; FEATURE:
; NAME/KEY: other
; LOCATION: 291..339
; IDENTIFICATION METHOD: blastn
; OTHER INFORMATION: identity 97
; OTHER INFORMATION: region 160..208
; OTHER INFORMATION: id T50032
; OTHER INFORMATION: est
; FEATURE:
; NAME/KEY: other
; LOCATION: 132..172
; IDENTIFICATION METHOD: blastn
; OTHER INFORMATION: identity 97
; OTHER INFORMATION: region 1..41
; OTHER INFORMATION: id T50032

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; OTHER INFORMATION: est
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 71..139
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 4.4
; OTHER INFORMATION: seq QFILLGTTVVTA/AL
US-08-905-223-188

Query Match      13.1%; Score 309; DB 3; Length 343;
Best Local Similarity 99.7%; Pred. No. 4.5e-75;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATCTTGGCGGCA CAGTGGCCACCGGGGCTCGCGCGCTCATGGAGCGGAGGCGGC 60
Db      |  |||||
QY      30  ATCTTGGCGGCA CAGTGGCCACCGGGGCTCGCGCGCTCATGGAGCGGAGGCGGC 89
Db      |  |||||

QY      61  CCTCGCTGTGCAGTTCATCCTCTCTGGGACACCTCTGTGGTCAACCGCGCCCTGTACT 120
Db      |  |||||
QY      90  CCTCGCTGTGCAGTTCATCCTCTCTGGGACACCTCTGTGGTCAACCGCGCCCTGTACT 149
Db      |  |||||

QY      121 CCGGTGTACCGGCAGAGCGCCGGGTCTCCCAAGAGCTCAAGGAGCTTAAAAAGTTCAAT 180
Db      |  |||||
QY      150 CCGGTGTACCGGCAGAGCGCCGGGTCTCCCAAGAGCTCAAGGAGCTTAAAAAGTTCAAT 209
Db      |  |||||

QY      181 TGGGTGAAGATTTAAAGAGTATCTTTCAGAAGCTCCAGGAAATCGTGCCCTTATGCTG 240
Db      |  |||||
QY      210 TGGGTGAAGATTTAAAGAGTATCTTTCAGAAGCTCCAGGAAATCGTGCCCTTATGCTG 269
Db      |  |||||

QY      241 TTATAGAAGGAGCTGTGGCTCTGTAAAGAACGCTTAAACGCCAGTTTGTGAAAACT 300
Db      |  |||||
QY      270 TTATAGAAGGAGCTGTGGCTCTGTAAAGAACGCTTAAACGCCAGTTTGTGAAAACT 329
Db      |  |||||

QY      301 GMAAGGGGT 310
Db      |  |||||

QY      330 GCAANGGGT 339
Db      |  |||||

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RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 1800 Alexandria Road, Suite 500
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22313-0299
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,463
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/07/935,313
;     FILING DATE:
;     APPLICATION NUMBER: EP 91 114 300.6
;     FILING DATE: 26-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME: BENT, Stephen A.
;       REGISTRATION NUMBER: 29,768
;       REFERENCE/DOCKET NUMBER: 30472/114, 1MMT

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486 GAAATTCAAAGAGTGAACTATTTTACTCTTTTACCTTCTCAATTAACRWANWAGAAW 427
383 AAAGATCATCATAGAGGACCAACACAGTGCCTTTTGACCTGTGCCCCACGAGGATGG 442
426 KKKMAGSMRACARAGTTTAAAGACWMAARRGWRARGRTGSGWKGGRWGRGMAAAK 367
443 CGTGGATGTGGCTGTGCGAGTGCTGAAGCCCTTGGACTCAGTGGATCTGGTCTTAGAGAC 502
366 MRMAAAGGSYCGMTSYTSGKOTGRKSGMTKREMMTYSGMWMTSYAKCTKTGKYYTGWK 307
503 TGTGTATGAGAAAGTTCCACCCCTCGAATTCAGTCTTCACCGATGTCTCATCGCCACTACAT 562
306 SKTRWTCTSRKYYMMWMSGWARSMKSWARSWYSGMAACWCMMSASAYRARRSMITGARRS 247
563 CAGCGGTAGCGGCCCAAGAGGCATCCAAGAGACCCGAGGAGATGCTGAAAGTGGGGGGCCAC 622
246 MPRAGAGWRARRRGGKRRGKS--SMRSMKMSMRMSAGKARMCRRMWSCRMYSYSCWG 189
623 CCTCAGACGGGTTGGCGAACTGTCTCTCGACAAACAATCTGTCTCGCGCTGACGCCCCCAA 682
188 SKMCKRGTCAKWRVARYAKRYASSMGKYMGMCRWCYAKCARMYGYRYSRSTGSRGM 129
683 ACAAGGCATCAGTACTATCTAAGAGCCAGGACTTCGACAGCCTGCTCGACAGGCAGGA 742
128 KYRERKYYMWKYMMSWMCYRGAAMYGMSARAYRMYASMSACKMCSRMMKMSWSMMW 69
743 GTCAGCGCTCAGGCTCTG 760
: : : : :
68 RCWRSRYRCWMSGKWYS 51

RESULT 5
US-09-074-912-3
; Sequence 3, Application US/09074912
; Patent No. 6057491
; GENERAL INFORMATION:
; APPLICANT: CIGAN, AMY L
; APPLICANT: CZAPLA, THOMAS H
; APPLICANT: FALLIS, LYNN
; APPLICANT: MEYER, TERRY E
; APPLICANT: MUNDELL, SCOTT A
; APPLICANT: SABUS, BRIAN
; APPLICANT: SCHUBERT, KAREL
; TITLE OF INVENTION: PROTEINS HAVING INSECTICIDAL ACTIVITIES
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: W. MURRAY SPRUILL (ALSTON & BIRD, LLP)
; STREET: 3605 GLENWOOD AVE.
; CITY: RALEIGH
; STATE: NC
; COUNTRY: USA
; ZIP: 27622
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,912
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: SPRUILL, W. MURRAY
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: 5718-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919 420 2202
; TELEFAX: 919 881 3175
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1227 base pairs
; TYPE: nucleic acid
;

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpc-F15
US-08-232-463-14

Query Match 2.5%; Score 59.6; DB 1; Length 7218;
Best Local Similarity 7.4%; Pred. No. 7,8e-06;
Matches 29; Conservative 207; Mismatches 156; Indels 0; Gaps 0;

QY 1860 TCCCTGGTTTCCTCTGGAGATGAGGCCACAGAGCCTCGCCTCTCTGAAGGACGCAGT 1919
DB ||| |||| | | | | | | | | | | | | | | | | | | | | | | | | | |
1000 TCCTTCGTTCGCATACGCTCACAGAATTAAATCCGAGCTTGCGTGCAGGTGCGAGGAGC 1059

QY 1920 GTGATGCCACTGGCCTAGTCTCTGGCTCACAGCTTCCTTCAAGGCTGTACAAGGA 1979
DB ||| :
1060 TTGCATYYY 1119

QY 1980 AAGCAGCGCGCTGCACCTCAGCATATGCCCTCTGGGCTCCCTCATCCAGCCGTC 2039
DB ||| :
1120 YY 1179

QY 2040 GCAGCTTTGACATCTTGGTGTAATACTCATGTCGCTTCTCTGTGTTACCCCTCCAGTAT 2099
DB ||| :
1180 YY 1239

QY 2100 TACCATTGCCCTCACCTGCCCTTGGTAGCTTCTTAGTCAAGACAGATGGGCTGTT 2159
DB ||| :
1240 YY 1299

QY 2160 TTCCCCACCTCGAGTAGTGGAGTCAATACACAGCTCTTTTTAATGCCCTTTTC 2219
DB ||| :
1300 YY 1359

QY 2220 TGCTCTGAATGTTTCATCTCTCGTCTCCCTTT 2251
DB ||| :
1360 YY 1391

RESULT 4
US-09-621-976-15639/c
Sequence 15639, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET 054PR2
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-15639

Query Match 1.9%; Score 44; DB 4; Length 505;
Best Local Similarity 16.2%; Pred. No. 0.037;
Matches 71; Conservative 170; Mismatches 195; Indels 2; Gaps 1;

QY 3223 GACACTTCAGGACCAAGATGGTGTGGAATCGAACCCACCCACCTTTGGAATGATTGTC 382

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "cDNA of Pentin-1 optimized
; ORIGINAL SOURCE: for enhanced expression"
; ORGANISM: Pentaclethra macroloba
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1227
US-09-074-912-3

Query Match
Best Local Similarity 1.8%; Score 43.2; DB 3; Length 1227;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 703 TAAGACGACGAGCTTCGACAGCCTGCTGACAGGAGGAGTGCAGCGTCAGGCTCTGGA 762
Db 158 TGATCTCTAAGCAGCTCTGAGGCGACCTCCAGAGGTGGGACTCCAGCGCAGGCTCGCG 217
QY 763 AGTGCTGGCGCTGGTTTGGCTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATCTCTCCGA 822
Db 218 AGTACTTCGAGCTGTGTGGCGGACCTCCACCGGCGCATCATCACCCTCTCTCACCG 277
QY 823 AGCAGTATCTGACGCGGAGGAGCGCTGCGC 854
Db 278 CCCCGACCGGAGAACAGGACCGCGCTC 309

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RESULT 6
US-09-290-136-3
; Sequence 3, Application US/09290136
; Patent No. 6339144
; GENERAL INFORMATION:
; APPLICANT: Cigan, Amy L.
; APPLICANT: Czapl, Thomas H.
; APPLICANT: Fallis, Lynn
; APPLICANT: Meyer, Terry E.
; APPLICANT: Mundell, Scott A.
; APPLICANT: Sabus, Brian
; APPLICANT: Schubert, Karel
; TITLE OF INVENTION: Proteins Having Insecticidal Activities and Methods of
; FILE REFERENCE: 5718-9A, 035718/180486
; CURRENT APPLICATION NUMBER: US/09/290.136
; EARLIER FILING DATE: 1999-04-13
; EARLIER FILING DATE: 09/074.912
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Pentaclethra macroloba
; FEATURE:
; OTHER INFORMATION: cDNA of Pentin-1 optimized for enhanced expression
; NAME/KEY: CDS
; LOCATION: (1)..(1227)
US-09-290-136-3

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Query Match
Best Local Similarity 1.8%; Score 43.2; DB 3; Length 1227;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 703 TAAGACGACGAGCTTCGACAGCCTGCTGACAGGAGGAGTGCAGCGTCAGGCTCTGGA 762
Db 158 TGATCTCTAAGCAGCTCTGAGGCGACCTCCAGAGGTGGGACTCCAGCGCAGGCTCGCG 217
QY 763 AGTGCTGGCGCTGGTTTGGCTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATCTCTCCGA 822
Db 218 AGTACTTCGAGCTGTGTGGCGGACCTCCACCGGCGCATCATCACCCTCTCTCACCG 277

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QY 823 AGCAGTATCTGACGCGGAGGAGCGCTGCGC 854
Db 278 CCCCGACCGGAGAACAGGACCGCGCTC 309

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RESULT 7

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US-09-270-767-10494
; Sequence 10494, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10494
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10494

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Matches 121; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 710 CCAGGACTTCGACAGCCTGCTGCAGAGGAGGAGTGCAGCGTCAGGCTCTGGAAGTGT 769
Db 364 CCACGAGGACGAGGTTCAGGTCTGATGGTGTGATGAGGACGTGTGCCCGGAGCGGTGT 423
QY 770 GCGCTGGTTTGGCTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATCTCCGGAAGCAGTA 829
Db 424 GGATGAGAAATGGTGTCTAAGAGCGTGCACAGTGCAGGCGCAAGGAGGAGGAGGAGCGGT 483
QY 830 TCTGACGCGGAGGAGCGCTGCGCCTCAACAGATGACGAGGAGGAGTTCAGGAGCATGA 889
Db 484 TCAGCGGAGGAGGAGTGCACAGTTCGCAACAGCGCAAGTGAAGGAGGCGAAGGAGGA 543
QY 890 GCGCCAGCTGCTGAGCGGAGCGCAAGCTGAGGAGGAGGAGTCTGAAGAGCGCTGTGT 949
Db 544 GCGGAGCGTGAAGCAGCAAGAACCTTGAGGCGAGGCGGCGCAAGCGGTGGATGC 603
QY 950 AGTGTGTCTGAGCA 963
Db 604 CGAGCGCTGGCCA 617

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RESULT 8

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US-08-728-323A-1
; Sequence 1, Application US/08728323A
; Patent No. 5948676
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A.
; APPLICANT: Russo, James J.
; APPLICANT: Edelman, Isidore S.
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Immediate Early Protein From Kaposi's
; TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,323A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3489
; US-08-728-323A-1

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Best Local Similarity 60.2%; Pred. No. 0.69;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
Db 1573 CAGCAGCAGGAGGCCACAGCAGCAGGAGGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632

QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCTGAGGACAGGAGAG 931
Db 1633 CAGCAGCAGGAGGCCACAGCAGCAGGAGGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1685

RESULT 9
US-09-298-568-1
; Sequence 1, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballestas, Mary E.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/298,568
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,422
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-298-568-1

Query Match 1.7%; Score 41; DB 3; Length 3489;
Best Local Similarity 60.2%; Pred. No. 0.69;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
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QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCTGAGGACAGGAGAG 931
Db 1633 CAGCAGCAGGAGGCCACAGCAGCAGGAGGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1685

RESULT 10
US-09-410-399-1
; Sequence 1, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Cotter, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; TITLE OF INVENTION: to Genomic Host DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-410-399-1

Query Match 1.7%; Score 41; DB 4; Length 3489;
Best Local Similarity 60.2%; Pred. No. 0.69;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
Db 1573 CAGCAGCAGGAGGCCACAGCAGCAGGAGGCCACAGCAGGAGGCCACAGCAGGAGGCCA 1632

QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCTGAGGACAGGAGAG 931
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RESULT 11
US-09-894-273-1
; Sequence 1, Application US/09894273
; Patent No. 6756203
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Ballestas, Mary E.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/894,273
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/109,422
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3489
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-894-273-1

Query Match 1.7%; Score 41; DB 4; Length 3489;
Best Local Similarity 60.2%; Pred. No. 0.69;
Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 819 CGGAAGCAGTATCTGCAGCGGCGAGGCGCTGCGCCCTCAAGCAGATGCAGGAGGATTC 878
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QY 879 CAGGAGCATGTAGCGGCCAGCTGCTGAGCGGAGCCAGCCTGAGGACAGGAGAG 931
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RESULT 12
US-08-770-379-20/c
; Sequence 20, Application US/08770379
; Patent No. 5849564
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/ GENERAL INFORMATION:
/ APPLICANT: Chang, Yuan
/ APPLICANT: Bohenzky, Roy A.
/ APPLICANT: Russo, James J.
/ APPLICANT: Edelman, Isidore S.
/ APPLICANT: Moore, Patrick S.
/ TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
/ TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper & Dunham LLP
/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/770,379
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 52342
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32207 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/
/ US-08-770-379-20
/
/ Query Match 1.7%; Score 41; DB 2; Length 32207;
/ Best Local Similarity 60.2%; Pred. No. 2.2;
/ Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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/ QY 819 CGGAAGCAGTATCTGCAGCGCAGGAGCGCTGCGCTCAAGCAGATGCAGGAGGATTC 878
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/ QY 879 CAGGAGCATGAGGCCAGCTGCTGAGCCGAGCCAGCTGAGGAGGAGGAG 931
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/ RESULT 13
/ US-08-757-669A-20/c
/ Sequence 20, Application US/08/757669A
/ Patent No. 6183751
/ GENERAL INFORMATION:
/ APPLICANT: Chang, Yuan
/ APPLICANT: Bohenzky, Roy A.
/ APPLICANT: Russo, James J.
/ APPLICANT: Edelman, Isidore S.
/ APPLICANT: Moore, Patrick S.
/ TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
/ TITLE OF INVENTION: SEQUENCES AND USES THEREOF
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper & Dunham LLP
/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
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/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/757,669A
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 45185-F
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32207 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/
/ US-08-757-669A-20
/
/ Query Match 1.7%; Score 41; DB 3; Length 32207;
/ Best Local Similarity 60.2%; Pred. No. 2.2;
/ Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
/
/ QY 819 CGGAAGCAGTATCTGCAGCGCAGGAGCGCTGCGCTCAAGCAGATGCAGGAGGATTC 878
/ Db 20424 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGGAGCCACAGCAGGAGCCCA 20365
/
/ QY 879 CAGGAGCATGAGGCCAGCTGCTGAGCCGAGCCAGCTGAGGAGGAGGAG 931
/ Db 20364 CAGCAGCAGGAGCCACAGCAGCAGGAGCCACAGCAGGAGCCCGGAGCCCGAGCG 20312
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/ RESULT 14
/ US-09-230-371A-20/c
/ Sequence 20, Application US/09230371A
/ Patent No. 6348586
/ GENERAL INFORMATION:
/ APPLICANT: Chang, Yuan
/ APPLICANT: Bohenzky, Roy A.
/ APPLICANT: Russo, James J.
/ APPLICANT: Edelman, Isidore S.
/ APPLICANT: Moore, Patrick S.
/ TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: 45185-G-PCT-US
/ CURRENT APPLICATION NUMBER: US/09/230,371A
/ CURRENT FILING DATE: 1999-11-17
/ PRIOR APPLICATION NUMBER: PCT/US97/13346
/ PRIOR FILING DATE: 1997-07-22
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 32207
/ TYPE: DNA
/ ORGANISM: Kaposi's sarcoma-associated herpesvirus
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/ US-09-230-371A-20
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/ Query Match 1.7%; Score 41; DB 3; Length 32207;
/ Best Local Similarity 60.2%; Pred. No. 2.2;
/ Matches 68; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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/ QY 819 CGGAAGCAGTATCTGCAGCGCAGGAGCGCTGCGCTCAAGCAGATGCAGGAGGATTC 878
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/ QY 879 CAGGAGCATGAGGCCAGCTGCTGAGCCGAGCCAGCTGAGGAGGAGGAG 931
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Fri Nov 12 12:23:28 2004

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Job time : 220 secs

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RESULT 15
US-08-366-276-1
; Sequence 1, Application US/08366276
; Patent No. 5534409
; GENERAL INFORMATION:
; APPLICANT: Groner, Bernd
; APPLICANT: Gouilleux, Fabrice
; APPLICANT: Wakao, Hiroshi
; TITLE OF INVENTION: Cytokine Regulated Transcription Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,276
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9409396.0
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scoot
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-19992/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2818 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 244..2625
; OTHER INFORMATION: /product= "mammary gland factor"

Query Match 1.7%; Score 40.8; DB 1; Length 2818;
Best Local Similarity 50.0%; Pred. No. 0.7;
Matches 102; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
QY 548 CATCGGCCCTACATCAGCGGTGAGCGGCCCAAGGCGATCCAAAGAGACCGAGGAGATGCT 607
Db 1125 CAGAGCGGAGCACCTCTGCCAGCAGCTGCCATCCCGGCCGCCGTGGAGGAGATGCTGC 1184
QY 608 GAAGGTGGGGGCCACCCCTCACAGGGTTGGCGAACTGGTCTCTGGACAACTCTGTCCG 667
Db 1185 TGAGGTCAAGCCACCATCAGGACATCATCTAGCCCTGGTGACCACGACATTCATCAT 1244
QY 668 CTTGACGCCGCCCAAGCAGTCAGTACTATCTAAGCAGCCAGGACTTCGACAGCCT 727
Db 1245 CGAAGCAGCGCCCTCAGGTCTCTGAAGACCCAGACCAAGTTCCGGGCCACCGTGGCCT 1304
QY 728 GCTGCAGAGGCGAGGTGAGCGT 751
Db 1305 GCTGTGGCGGGAAGCTGAACGT 1328

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2004, 17:32:53 ; Search time 196 Seconds
(without alignments)
1033.326 Million cell updates/sec

Title: US-09-978-360A-437

Perfect score: 1831
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt.02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	1672	91.3	352	2	Q8BHF2
6	1667	91.0	352	2	Q9DCV9
7	1277.5	69.8	352	2	Q6NTT6
8	1277.5	69.8	353	2	Aah68869
9	442.5	24.2	338	2	Q9VZJ9
10	436	23.8	339	2	Q7Q6A1
11	391.5	21.4	283	2	Q6PBA9
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17	201	11.0	383	2	Q9SVH3
18	166	9.1	376	2	Q99KR6
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23	163	8.9	372	2	Q969K3
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28	156	8.5	654	2	Q7TOK2
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36	155.5	8.5	723	2	Q96GT5
37	155.5	8.5	723	2	AAQ89189
38	151	8.2	319	2	Q8T0T5
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45	143.5	7.8	355	2	Q8NHW0

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ALIGNMENTS

RESULT 1
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DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein FLJ12875 (Hypothetical protein DKFZp762M0911).
GN Name=FLJ12875; Synonyms=DKFZp762M0911;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.F., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Hale S., Garcia A.M., Guernsey J., Lander A., Rozen S., White O., Botstein D., Finkbeiner S., Schaefer C.F., Gibbs R.A., Fanev J., Helton E., Kettman M., Madan A., Young A.C., Shevchenko Y., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Kravinsky M.I., Shalaka U., Small U., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RA Blum H., Baersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC014010; AAH14010.1; -.

DR EMBL; BC010101; AAH10101.1; -;
 DR EMBL; AL333989; CAD38745.1; -;
 DR GO; GO:0004871; F:signal transducer activation; IMP.
 DR GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-kappaB; IMP.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 352 AA; 39800 MW; 6EF2B8B8BFC1801F CRC64;
 Query Match 100.0%; Score 1831; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 2.6e-127; Indels 0; Gaps 0;
 Matches 352; Conservative 0; Mismatches 0;
 QY 1 MESGGRPSLCQFILLGTTTSVVTAAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 Db 1 MESGGRPSLCQFILLGTTTSVVTAAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 QY 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKVMWNRTHLWDCSKIIHQ 120
 Db 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKVMWNRTHLWDCSKIIHQ 120
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLTETVYKHPHSIQSFTDVIGHYISGERPK 180
 Db 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLTETVYKHPHSIQSFTDVIGHYISGERPK 180
 QY 181 GIOETEEMLKVGATLTGVELVLDNNSVRLQPPQKQMYLLSQDPSLLQKQESSVRLW 240
 Db 181 GIOETEEMLKVGATLTGVELVLDNNSVRLQPPQKQMYLLSQDPSLLQKQESSVRLW 240
 QY 241 KVLALVFGFATCATLFFILRKQYLQRLKQERLRLKQMOEFQEHQAQLLSRAKPEDRESLKS 300
 Db 241 KVLALVFGFATCATLFFILRKQYLQRLKQERLRLKQMOEFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSPKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLNS 352
 Db 301 ACVCLSSPKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLNS 352
 RESULT 2
 Q72431 PRELIMINARY; PRT; 352 AA.
 ID Q72431
 AC Q72431
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative NF-kB activating protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RC MEDLINE=22646590; PubMed=12761501;
 RA Matsuda A., Suzuki Y., Honda G., Muramatsu S., Mutsuzaki O.,
 RA Nagano Y., Doi T., Shimotohno K., Harada T., Nishida E., Hayashi H.,
 RA Sugano S.;
 FT "Large-scale identification and characterization of human genes that
 activate NF-kappaB and MAPK signaling pathways.";
 RL Oncogene 22:3307-3318(2003).
 DR EMBL; AB097015; BAC77368.1;
 DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; F:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS0089; ZF_RING_2; 1.
 SQ SEQUENCE 352 AA; 39784 MW; 6EF2B8B8BFC1801F CRC64;
 Query Match 99.6%; Score 1824; DB 2; Length 352;
 Best Local Similarity 99.7%; Pred. No. 8.5e-127;

Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MESGGRPSLCQFILLGTTTSVVTAAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 Db 1 MESGGRPSLCQFILLGTTTSVVTAAALYSVYRQKARVSQELGAKKVKHGLGDLKSLSEAPG 60
 QY 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKVMWNRTHLWDCSKIIHQ 120
 Db 61 KCVPVAVIEGAVRSVKETLNSQFVENCCKGVQRLTLQEHKVMWNRTHLWDCSKIIHQ 120
 QY 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLTETVYKHPHSIQSFTDVIGHYISGERPK 180
 Db 121 TMTVPFDLVPHEDGVDAVAVRLKPLDSVDLGLTETVYKHPHSIQSFTDVIGHYISGERPK 180
 QY 181 GIOETEEMLKVGATLTGVELVLDNNSVRLQPPQKQMYLLSQDPSLLQKQESSVRLW 240
 Db 181 GIOETEEMLKVGATLTGVELVLDNNSVRLQPPQKQMYLLSQDPSLLQKQESSVRLW 240
 QY 241 KVLALVFGFATCATLFFILRKQYLQRLKQERLRLKQMOEFQEHQAQLLSRAKPEDRESLKS 300
 Db 241 KVLALVFGFATCATLFFILRKQYLQRLKQERLRLKQMOEFQEHQAQLLSRAKPEDRESLKS 300
 QY 301 ACVCLSSPKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLNS 352
 Db 301 ACVCLSSPKSCVFLGCHVCSCTCYRALPEPKKPCICROAITRVIPLNS 352
 RESULT 3
 Q9H9B5 PRELIMINARY; PRT; 352 AA.
 ID Q9H9B5
 AC Q9H9B5
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ12875.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=14702039;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakumaki B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Ozaki Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Takahashi Y., Nakagawa K.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamashita R.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Iwashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).

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DR EMBL; AK029377; BAB14317.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
SQ SEQUENCE 352 AA; 39717 MW; C19F150D278C2DA9 CRC64;

Query Match          99.3%; Score 1818; DB 2; Length 352;
Best Local Similarity 99.7%; Pred. No. 2.4e-126;
Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKKVKHLGEDLKSILSEAPG 60
Db 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKKVKHLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCNGVIOQLTLQEHKVMWNRTHLWDCSKIIHOR 120
Db 61 KCVPAVIEGAVRSVKETLNSQFVENCNGVIOQLTLQEHKVMWNRTHLWDCSKIIHOR 120
QY 121 TINTVPDLVPHEDGVAVRVLPKPLDSVDLGLTVEYKFPSPISQFTDVIHYISGERPK 180
Db 121 TINTVPDLVPHEDGVAVRVLPKPLDSVDLGLTVEYKFPSPISQFTDVIHYISGERPK 180
QY 181 GIQTEEMLVKGATLTVGVELVLDNNSVRLQPPKQGMQYLLSSQDFDLSLQRESSVRLW 240
Db 181 GIQTEEMLVKGATLTVGVELVLDNNSVRLQPPKQGMQYLLSSQDFDLSLQRESSVRLW 240
QY 241 KVLALVFGFATCATLFFILRKQYLQORERLQKQEEFQHEAQLLSRAKPEDRESLKS 300
Db 241 KVLALVFGFATCATLFFILRKQYLQORERLQKQEEFQHEAQLLSRAKPEDRESLKS 300
QY 301 ACVCLSFKSCVFLECGHVCSTECYRALPEPKKCPICRQAITRVIPLVNS 352
Db 301 ACVCLSFKSCVFLECGHVCSTECYRALPEPKKCPICRQAITRVIPLVNS 352

RESULT 4
Q8VCM5 ID Q8VCM5 PRELIMINARY; PRT; 352 AA.
AC Q8VCM5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RIKEN cDNA 0610009K11.
GN Name=0610009K11Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019516; AAH19516.1; -.
DR HSSP; P38398; 1JM7.
DR MGD; MGI:1915600; 0610009K11Rik.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
SQ SEQUENCE 352 AA; 39821 MW; F3FE5D4771E0B140 CRC64;

Query Match          91.4%; Score 1673; DB 2; Length 352;
Best Local Similarity 90.1%; Pred. No. 1.3e-115;
Matches 317; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKKVKHLGEDLKSILSEAPG 60
Db 1 MESGRPSLCQIFLLGTTSVTAALYSVYRQKARVSOELKGAKKVKHLGEDLKSILSEAPG 60
QY 61 KCVPAVIEGAVRSVKETLNSQFVENCNGVIOQLTLQEHKVMWNRTHLWDCSKIIHOR 120
Db 61 KCVPAVIEGAVRSVKETLNSQFVENCNGVIOQLTLQEHKVMWNRTHLWDCSKIIHOR 120
QY 121 TINTVPDLVPHEDGVAVRVLPKPLDSVDLGLTVEYKFPSPISQFTDVIHYISGERPK 180
Db 121 TINTVPDLVPHEDGVAVRVLPKPLDSVDLGLTVEYKFPSPISQFTDVIHYISGERPK 180
QY 181 GIQTEEMLVKGATLTVGVELVLDNNSVRLQPPKQGMQYLLSSQDFDLSLQRESSVRLW 240
Db 181 GIQTEEMLVKGATLTVGVELVLDNNSVRLQPPKQGMQYLLSSQDFDLSLQRESSVRLW 240
QY 241 KVLALVFGFATCATLFFILRKQYLQORERLQKQEEFQHEAQLLSRAKPEDRESLKS 300
Db 241 KVLALVFGFATCATLFFILRKQYLQORERLQKQEEFQHEAQLLSRAKPEDRESLKS 300
QY 301 ACVCLSFKSCVFLECGHVCSTECYRALPEPKKCPICRQAITRVIPLVNS 352
Db 301 ACVCLSFKSCVFLECGHVCSTECYRALPEPKKCPICRQAITRVIPLVNS 352

RESULT 5
Q8BHF2 ID Q8BHF2 PRELIMINARY; PRT; 352 AA.
AC Q8BHF2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A830089D08 product:hypothetical RING finger containing
DE protein, full insert sequence (Mus musculus 0 day neonate head cDNA,
DE RIKEN full-length enriched library, clone:4831423H02
DE product:hypothetical RING finger containing protein, full insert
DE sequence) (Mus musculus adult male liver tumor cDNA, RIKEN full-length
DE enriched library, clone:C730031H18 product:hypothetical RING finger
DE containing protein, full insert sequence).
GN Name=0610009K11Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=99279253; PubMed=10349636;

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RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex, Head, and Liver;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Tanaka Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head, and Liver;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Tanaka Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Tanaka Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[9]
RP EMBL; AK040088; BAC31768.1; -
DR EMBL; AK076419; BAC36332.1; -
DR HSP; P38398; IJM7
DR MGD; MGI:1915600; 0610009K1Rik.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PSS0089; ZF_RING_2; 1.
DR Hypothetical protein.
KW SEQUENCE 352 AA; 39835 MW; 252530F1BD917871 CRC64;
Query Match 91.3%; Score 1672; DB 2; Length 352;
Best Local Similarity 89.8%; Pred. No. 1.5e-115;
Matches 316; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
Qy 1 MESGSRPCLQCFILLGTTTAAALYSVYRQKARVSQELKGAQKVLHGLKSLSEAPG 60
Db 1 MESGSRPCLQCFILLGTTTAAALYSVYRQKARVSQELKGAQKVLHGLKSLSEAPG 60
Qy 61 KCVPYAVTEGAVRSVKETLNSQFVENCCKGVIRLTLOEHKMWNRTHLWDCSKIIHQ 120
Db 61 KCVPYAVTEGAVRSVKETLNSQFVENCCKGVIRLTLOEHKMWNRTHLWDCSKIIHQ 120
Qy 121 TTTVPFDLVPHEDGVAVRVLPKLDSDVLDLGLTVEYKFPSPISQFTDVI GHYISGERPK 180
Db 121 TTTVPFDLVPHEDGVAVRVLPKLDSDVLDLGLTVEYKFPSPISQFTDVI GHYISGERPK 180
Qy 181 GIQTEEMLVKVGATLTGVGELVLDNNSVRLPPQKQMOYLLSSQDFDLSLORQESSVRLW 240
Db 181 GIQTEEMLVKVGATLTGVGELVLDNNSVRLPPQKQMOYLLSSQDFDLSLORQESSVRLW 240
Qy 241 KVLALVFGFATCATLFFTLRKQYLORQERLQKQOEFOHEAQLLGRAPKPEDRESLKS 300
Db 241 KVLALVFGFATCATLFFTLRKQYLORQERLQKQOEFOHEAQLLGRAPKPEDRESLKS 300
Qy 301 ACVCLSLFSCVFCLECHGVSCCTCYRALPEPKPCICRQAITRVIPLYS 352
Db 301 ACVCLSLFSCVFCLECHGVSCCTCYRALPEPKPCICRQAITRVIPLYS 352
RESULT 6
Q9DCV9 PRELIMINARY; PRT; 352 AA.
AC Q9DCV9; (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Mus musculus adult male kidney cDNA, RIKEN full-length enriched
DE library, clone:0610009K11 product:hypothetical RING finger containing
DE protein, full insert sequence.
GN Name=0610009K1Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Kidney;
The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002)."
[4]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishihira T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Tagawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RL sequencing pipeline with 384 multichannel sequencer.";
Genome Res. 10:1757-1771 (2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=20530913; PubMed=11076861;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojiya Y., Konno H., Kouma M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numasaki R.,
RA Okazaki Y., Okido T., Owa C., Saio H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa Y., Takahashi F., Tanaka T.,
RA Tejima Y., Toyota T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AK02416; BAB22084.1; -;
DR HSPF; P38398; 10M7.
DR MGP; MG1.1915600; 0610009K1IRIK.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING_1.
KW Hypothetical protein_Znf_ring_1.
SQ SEQUENCE 352 AA; 3988 MW; 29933D46BD9165C6 CRC64;

Query Match 91.0%; Score 1667; DB 2; Length 352;
Best Local Similarity 89.5%; Pred. No. 3 6e-115;
Matches 315; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MESGSRPSLCQIFLLGTTSVTAALYSVYRKARYSDELKAKVKHLGEDLKSLSEAPG 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MESGSRPSLCQIFLLGTSSMTAVLSIYRQAQVAQLKGAKKTHLGEDLKSLSEAPG 60

QY 61 KCVPYAVIEGASRVSKETLNQSVENCCKVIORLTLOEHKMWNPTTLWNDSCSIHQH 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 KCVPYAVIEGASRVSKETLNQSVENCCKVIORLSLQEHKMWNPTTLWNDYSKIHQH 120

QY 121 TNTVPFDLPHPDGVDVAVRLKPLDSVDGLGETVYEKPHFSIQSTDVIGHYISGERPK 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 TNTVPFDLPHPDGVDVAVRLKPLDSVDGLGETVYEKPHFSIQSTDVIGHYISGERPK 180

RA Jones S.J., Marra M.A.;

RA Cherry J.M., Cawley S., Danke C., Davenport E.B., Lawrence
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.

RA Cherry J.M., Cawley S., Danke C., Davenport E.B., Lawrence
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.

FT	NON TER	1	283	AA;	31798	MW;	CD3C66BB7B68350C	CRC64;	
SEQ	SEQUENCE								
	Query Match		21.4%;	Score	391.5;	DB 2;	Length	283;	
	Best Local Similarity		37.2%;	Pred. No.	8.1e-21;	Indels	7;	Gaps	5;
	Matches		92;	Conservative	45;	Mismatches	103;		
QY		13	ILLGTTSVVTAALYSVYVROKARVSQELKGAKKVHVGEDLKSILSEAPGKCVPIAVIEGAV	72					
Db		25	ICAGSCFAFGSLFYKLYSDKRLVQKLKEIPNFQPDHLLRLILNASSNKRCLHYVAVEGLV	84					
QY		73	RSVKETLNSQFVENCXGVQIQRLLQLQEHQVMVNRTHLLWDCSKLIH--QRKNTTVPFDLV-	129					
Db		85	QAVGEPISSQYVPRCHGVIQKITVHEHWKYNSLLKSW--VSKRNQQTNTTVPFVLVQ	142					
QY		130	PHEDGVDVAVRVLKPLDSDVLGLLETVEYKTHPSIQSFDTDIGHYISGERPKGIQETEML	189					
Db		143	PGSFISDVCVRVDSPLSAGDGFQQVHRVRVNAKEGLMDAVLGIISGEKPIALEERDLL	202					
QY		190	KVGATLTGVGELVLDNNSV--RLQPPKQGMQYVSSQDPSDLLQRQESVRLKVLALVFG	248					
Db		203	RVGVPLTAFGELVLEQEKIMRIQPKDGRGFLVLPDSYNFPMQRHQSNNVMKGLTVLFG	262					
QY		249	FATCATL	255					
Db		263	L-TGSTL	268					

RESULT 12

AAH59797	PRELIMINARY;	PRT;	283 AA.
ID	AAH59797		
AC	AAH59797;		
DT	03-MAR-2004 (TReMBLrel. 27, Created)		
DT	03-MAR-2004 (TReMBLrel. 27, Last sequence update)		
DT	03-MAR-2004 (TReMBLrel. 27, Last annotation update)		
DE	LOC402879 protein (Fragment).		
GN	LOC402879.		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;		
OC	Cyprinidae; Danio.		
OX	NCBI_TaxID=7955;		
RI	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Kidney;		
RC	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villaalon D., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).		
RI	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Strausberg R.;		
RL	Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC059797; AAH59797.1; -.		
FT	NON TER 1 1		

[illegible]

Fri Nov 12 12:23:32 2004

Best Local Similarity 27.3%; Pred. No. 2e-11;
Matches 97; Conservative 64; Mismatches 136; Indels 58; Gaps 19;
QY 24 ALYVVRQKARVSOELGAKVHLGDLKILSEAPGKCPVYAVIEGAVRSVKETLNSQF 83
Db 15 ALYLLTRSTGR---DIKSTRVYQKLEQLV-EVESKVVPLII-----AVSGDVGSET 64
QY 84 VENCK-----GVIOQLTLQEHKVMNRTHLWDCSKIIHQRTNTVPFDLVPHEHDGVDVA 138
Db 65 PIKCEHSYVLGVFLKRT-AEQOVLRRNRWFSWVRNSTLMQPMTEKVEPWYL---DDGTG-- 118
QY 139 VRVLKPLDSVDLGL-----ETVYEKFPHSIQSFTDVIGHYISGRPKGIQETEMLVKVA 193
Db 119 -RVNVDVSQGLGALTGVSDVFEKAP-VSLVQAGALG-YLKGFKILGVRHVERVPIGT 175
QY 194 TLTVGELVLDN-NSVRLQPPKQGMYYLSSQDSDLQROESSVRLWKVLAL---VFGF 249
Db 176 PLTVVGEAVRDGMGNVRIOKPEQG-PFYVTIPLDLQILSKGLDLSRRFKYASMGITVLGV 234
QY 250 ATCA--TLFFTLRK--QVLOQER-LRLKQMOEEFQHEAQLLSRAKPEDRES----- 297
Db 235 ILISKPVIEYILKRIEDTLERRRQFALKRVVD-----AAARRAKPVTGGSGTGRD 287
QY 298 --LKSACVVCLSSPKSCVFLGCHVSCTECYRALPEPKKCPICQAITRVIPLY 350
Db 288 GDTPLCVCLDQKYNATAFVCGHMCCTPCSLQ---RTCPLCRERIQQVLKIY 339

Search completed: November 6, 2004, 17:42:25
Job time : 200 secs

SQ SEQUENCE 338 AA; 37729 MW; BA5598FB4C0D296C CRC64;
Query Match 14.6%; Score 267.5; DB 2; Length 338;
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Matches 97; Conservative 66; Mismatches 133; Indels 57; Gaps 20;
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Db 15 ALYLLTRSTGR---DIKSTRVYQKLEQLV-EVESKVVPLII-----AVSGDVGSET 64
QY 84 VENCK-----GVIOQLTLQEHKVMNRTHLWDCSKIIHQRTNTVPFDLVPHEHDGVDVA 138
Db 65 PIKCEHSYVLGVFLKRT-AEQOVLRRNRWFSWVRNSTLMQPMTEKVEPWYL---DDGTG-- 118
QY 139 VRVLKPLDSVDLGL-----ETVYEKFPHSIQSFTDVIGHYISGRPKGIQETEMLVKVA 193
Db 119 -RVNVDVSQGLGALTGVSDVFEKAP-VSLVQAGALG-YLKGFKILGVRHVERVPIGT 175
QY 194 TLTVGELVLDN-NSVRLQPPKQGMYYLSSQDSDLQROESSVRLWKVLAL---VFGF 249
Db 176 PLTVVGEAVRDGMGNVRIOKPEQG-PFYVTIPLDLQILSKGLDLSRRFKYASMGITVLGV 234
QY 250 ATCA--TLFFTLRK--QVLOQER-LRLKQMOEEFQHEAQLLSRAKPEDRES-----EDRES 297
Db 235 ILISKPVIEYILKRIEDTLERRRQFALKRVVD-----AAARRAKPVTGGSGTGRDGT 287
QY 298 LKSACVVCLSSPKSCVFLGCHVSCTECYRALPEPKKCPICQAITRVIPLY 350
Db 288 -PDLCVCLDQKYNATAFVCGHMCCTPCSLQ---RTCPLCRERIQQVLKIY 336

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AC Q9LQ59;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE T30816.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]_TaxID=3702;
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Dunn P., Khan S., Kim C., Shinn P.,
RA Altati H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Lueros S.,
RA Rowley D., Schwartz J., Toriumi M., Vyotskaia V., Yu G., Davis R.W.,
RA Federspiel N.A., Theologis A., Ecker J.R.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Chao Q., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altati H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AC009317; AAF79749.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR001841; Znf_ring.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
SQ SEQUENCE 341 AA; 38017 MW; 6511F8370A7B5450 CRC64;

Query Match 14.5%; Score 266; DB 2; Length 341;

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 CompuGen Ltd.
 OM nucleic - nucleic search, using sw model
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 (without alignments)
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 Title: US-09-978-360A-32
 Perfect score: 2356
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 Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 3611042 seqs, 2692057975 residues
 Total number of hits satisfying chosen parameters: 7222084
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2356	100.0	2356	11	US-09-978-360A-32
2	2356	100.0	2356	15	US-10-315-664-55
3	2338.4	99.3	2413	16	US-10-169-395-112
4	2336.8	99.2	2401	15	US-10-024-298A-76
5	2336.8	99.2	2401	15	US-10-042-211A-76
6	2336.8	99.2	2401	16	US-10-617-217A-76
7	2336.8	99.2	2401	18	US-10-024-298A-76
8	2335.2	99.1	2401	15	US-10-024-298A-74
9	2335.2	99.1	2401	15	US-10-042-211A-74
10	2335.2	99.1	2401	16	US-10-617-217A-74
11	2335.2	99.1	2401	18	US-10-024-298A-74
12	2330.8	98.9	2446	9	US-09-764-864-14

13	2217	94.1	2377	16	US-10-221-625-132	Sequence 132, Appl
14	1766	75.0	1791	9	US-09-764-864-475	Sequence 475, Appl
15	1751.4	74.3	1780	16	US-10-264-237-1275	Sequence 1275, Ap
16	1059	44.9	1059	16	US-10-169-395-102	Sequence 102, Appl
17	435	18.5	435	15	US-10-206-901B-36	Sequence 36, Appl
18	363	15.4	374	9	US-09-983-965-5476	Sequence 1321, Ap
19	290.8	12.3	398	9	US-09-983-965-5476	Sequence 5476, Ap
20	195.2	8.3	260	16	US-10-242-535A-4864	Sequence 4864, Ap
21	195.2	8.3	260	16	US-10-085-783A-2905	Sequence 2905, Ap
22	162.4	6.9	175	16	US-10-242-535A-2905	Sequence 2905, Ap
23	162.4	6.9	175	16	US-10-085-783A-2905	Sequence 11630, A
24	105.6	4.5	167	9	US-09-783-590-11630	Sequence 11630, A
25	60	2.5	60	10	US-09-908-975-13122	Sequence 13122, A
26	47.2	2.0	88232	13	US-10-087-192-1599	Sequence 1699, Ap
27	45.8	1.9	1239	15	US-10-214-446-35	Sequence 35, Appl
28	45.8	1.9	18438	15	US-10-156-761-2886	Sequence 2886, Ap
29	45.8	1.9	125746	15	US-10-156-761-15102	Sequence 15102, A
30	45.8	1.9	9025608	15	US-10-156-761-1	Sequence 1, Appli
31	45.4	1.9	412	9	US-09-983-965-4755	Sequence 4755, Ap
32	44.4	1.9	2436	15	US-10-369-493-43090	Sequence 43090, A
33	43	1.8	2076	15	US-10-156-761-4305	Sequence 4305, Ap
34	43	1.8	3710	17	US-10-322-281-599	Sequence 599, Ap
35	43	1.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
36	42.8	1.8	1716	16	US-10-260-238-1227	Sequence 1227, Ap
37	42.8	1.8	1737	17	US-10-437-963-8794	Sequence 8794, Ap
38	42.4	1.8	2511	17	US-10-437-963-8794	Sequence 8794, Ap
39	42.2	1.8	2556	18	US-10-425-115-88564	Sequence 88564, A
40	42	1.8	594	14	US-10-123-155-10	Sequence 10, Appl
41	42	1.8	594	15	US-10-146-731-10	Sequence 10, Appl
42	42	1.8	594	15	US-10-140-472-10	Sequence 10, Appl
43	42	1.8	594	15	US-10-141-761-10	Sequence 10, Appl
44	42	1.8	594	15	US-10-142-885-10	Sequence 10, Appl
45	42	1.8	594	15	US-10-158-790-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-978-360A-32
 ; Sequence 32, Application US/09978360A
 ; Publication No. US20040110939A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
 ; APPLICANT: Duclert, Aymeric
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Jobert, Severin
 ; APPLICANT: Clusel, Catherine
 ; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
 ; FILE REFERENCE: 56.USA.CIP
 ; CURRENT APPLICATION NUMBER: US/09/978,360A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: US 60/066,677
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: US 60/069,957
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: US 60/074,121
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: US 60/081,563
 ; PRIOR FILING DATE: 1998-04-13
 ; PRIOR APPLICATION NUMBER: US 60/096,116
 ; PRIOR FILING DATE: 1998-08-10
 ; PRIOR APPLICATION NUMBER: US 60/099,273
 ; PRIOR FILING DATE: -09-04
 ; PRIOR APPLICATION NUMBER: US 09/191,997
 ; PRIOR FILING DATE: 1998-11-13
 ; PRIOR APPLICATION NUMBER: US 09/215,435
 ; PRIOR FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: PCT/IB98/02122
 ; PRIOR FILING DATE: 1998-12-17
 ; PRIOR APPLICATION NUMBER: US 09/247,155
 ; PRIOR FILING DATE: 1999-02-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.


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QY 1801 TCTGGTTTCCCACTGGCCCTGATTTGAACCTCTGCCACTTGGGAGAGCTCGGGTGT 1860
Db 1801 TCTGGTTTCCCACTGGCCCTGATTTGAACCTCTGCCACTTGGGAGAGCTCGGGTGT 1860
QY 1861 CCTGGTTTTCCTCTCCCTGGGAATGAGGCGAGAGGCTCGCCCTCTCTGAAGGACGAGTG 1920
Db 1861 CCTGGTTTTCCTCTCCCTGGGAATGAGGCGAGAGGCTCGCCCTCTCTGAAGGACGAGTG 1920
QY 1921 TGGATGCCACTGGCCTAGTCTCTGGCCTCACAGCTTCCTTGAAGCTGTCAAGGAA 1980
Db 1921 TGGATGCCACTGGCCTAGTCTCTGGCCTCACAGCTTCCTTGAAGCTGTCAAGGAA 1980
QY 1981 AAGCAGCGGCTGGCACTGGAGCATATGCCCCCTTGGGGCTCCCTCATCCAGCCGCTG 2040
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QY 2341 AAAAAAAAAAAAAA 2356
Db 2341 AAAAAAAAAAAAAA 2356
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RESULT 2

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US-10-315-664-55
; Sequence 55, Application US/10315664
; Publication No. US20030203377A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: GNSSET.050CP3
; CURRENT APPLICATION NUMBER: US/10/315,664
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/599,360
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 55
; LENGTH: 2356
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..1097
; FEATURE:
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; NAME/KEY: sig_peptide
; LOCATION: 42..110
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.40
; OTHER INFORMATION: seq QFILLGTTTSVVA/AL
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 2323..2328
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2341..2356
US-10-315-664-55

Query Match 100.0%; Score 2356; DB 15; Length 2356;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCCCGCTCATGGAGAGCGAGGGCGGC 60
Db 1 ATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCCCGCTCATGGAGAGCGAGGGCGGC 60
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Db 61 CTTGCTGTGCCAGTTCATCTCTCTGGGACACCACTCTGTGTGTCACCGCCGCTGTACT 120
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Db 121 CCGTGTACCGGCGAGAGGCCCGGCTCTCCCAAGAGCTCCAGGAAATGCGTGCTTATGCTG 180
QY 181 TGGGTGAAGATTTAAAGAGTATTTTTCAGAGCTCCAGGAAATGCGTGCTTATGCTG 240
Db 181 TGGGTGAAGATTTAAAGAGTATTTTTCAGAGCTCCAGGAAATGCGTGCTTATGCTG 240
QY 241 TTATAGAGGAGCTGTGCGGTCTGTAAAGAAACGCTTAAACAGCAGTTTGTGAAAACT 300
Db 241 TTATAGAGGAGCTGTGCGGTCTGTAAAGAAACGCTTAAACAGCAGTTTGTGAAAACT 300
QY 301 GCAAGGGGGTAAATTCAGCGGCTGACATTTCAGGAGCACAAGATGTTGGATCGAACCA 360
Db 301 GCAAGGGGGTAAATTCAGCGGCTGACATTTCAGGAGCACAAGATGTTGGATCGAACCA 360
QY 361 CCCACCTTTGGAATGATTTGCTCAAAGATCAITTCATCAGAGGACCAACACAGTGCCTTTG 420
Db 361 CCCACCTTTGGAATGATTTGCTCAAAGATCAITTCATCAGAGGACCAACACAGTGCCTTTG 420
QY 421 ACCTGTGCCCCACGAGATGCGGTGATGTGGTGTGCGAGTGTGAAGCCCTGGACT 480
Db 421 ACCTGTGCCCCACGAGATGCGGTGATGTGGTGTGCGAGTGTGAAGCCCTGGACT 480
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Db 541 CCGATGTCTCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCATCCAAAGAGACCGAGG 600
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Db 601 AGATGCTGAAGTGGGGGCCACCTCACAGGGTTGGCGAACTGGTCTTGGAAACAACACT 660
QY 661 CTGTCCGCTTCAGCGCCGCCAAACAGGATGAGTACTATCTTAAGCAGCAGGACTTCG 720
Db 661 CTGTCCGCTTCAGCGCCGCCAAACAGGATGAGTACTATCTTAAGCAGCAGGACTTCG 720
QY 721 ACAGCCTGTCTCAGAGGCGAGGAGTGGAGCTCTGGAAGTGTGCGGCTGCTGCTGCTG 780
Db 721 ACAGCCTGTCTCAGAGGCGAGGAGTGGAGCTCTGGAAGTGTGCGGCTGCTGCTGCTG 780
QY 781 TTGGCTTTGCCACATGTGCCACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
Db 781 TTGGCTTTGCCACATGTGCCACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
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Fri Nov 12 12:23:29 2004

us-09-978-360a-32.rnpb

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1681 CAGCTGTGTAGAGGACAAAGAAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1740
1741 CCGGCGCCCGGCGCAACAGATTAAGAGAGATCATGTGAAGGAGGAGTGTGTCAGGAGCC 1800
1741 CCGGCGCCCGGCGCAACAGATTAAGAGAGATCATGTGAAGGAGGAGTGTGTCAGGAGCC 1800
1801 TCCTGGTTTCCGCACTGCGCTGATTTGAATCTCTGCACTTGGAGAGCTCGGGGTGGT 1860
1801 TCCTGGTTTCCGCACTGCGCTGATTTGAATCTCTGCACTTGGAGAGCTCGGGGTGGT 1860
1861 CCCTGGTTTTTCCCTTCTGGAGATGAGGCGGAGAGGCTCGCTCTTGAAGAGCAGTGT 1920
1861 CCCTGGTTTTTCCCTTCTGGAGATGAGGCGGAGAGGCTCGCTCTTGAAGAGCAGTGT 1920
1921 TGGATGCACTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980

1921 TGGATGCACTGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
1981 AAGAGCGCGCTGGCACCCTGAGCATATGCTTCTTGGGGCTCCCTCATCCAGCCCGTGC 2040
1981 AAGAGCGCGCTGGCACCCTGAGCATATGCTTCTTGGGGCTCCCTCATCCAGCCCGTGC 2040
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2221 GCCTCTGAATGTTTATCT 2280
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2341 AAAAAAAAAAAAAAAAAA 2356
2341 AAAAAAAAAAAAAAAAAA 2356

RESULT 3

US-10-169-395-112
; Sequence 112, Application US/10169395
; Publication No. US20040034192A1
; GENERAL INFORMATION:
; APPLICANT: KATO, Seishi
; APPLICANT: KIMURA, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING
; TITLE OF INVENTION: THESE PROTEINS
; FILE REFERENCE: 01997.015100.US
; CURRENT APPLICATION NUMBER: US/10/169,395
; CURRENT FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: JP 2000-585
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-588
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: JP 2000-2299
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-26862
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: JP 2000-58367
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/JP00/09359
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 150
; SEQ ID NO 112
; LENGTH: 2413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(1173)
US-10-169-395-112

Query Match 99.3%; Score 2338.4; DB 16; Length 2413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 74 ATCCTTGGCGCACAGTGGCGGCTCGCGGCTCATGAGAGCGAGGCGGC 133

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 Db 134 CCTCGCTGTGCCAGTTTCATCTCTGGGCACACCTCTGTGGTCACCGCCGCTGTACT 193
 QY 121 CCGTGTACCGGAGAGGCCGGGTCTCCAAAGAGTCAAGGGAGCTTAAAAAGTTCAIT 180
 Db 194 CCGTGTACCGGAGAGGCCGGGTCTCCAAAGAGTCAAGGGAGCTTAAAAAGTTCAIT 253
 QY 181 TGGGTGAAGATTAAAGAGTATCTTTCAAGAGCTCCAGAAAAATGCGTCTTATGCTG 240
 Db 254 TGGGTGAAGATTAAAGAGTATCTTTCAAGAGCTCCAGAAAAATGCGTCTTATGCTG 313
 QY 241 TTATAGAAGAGCTGTGCGGTCTGTAAAGAAACGCTTAAACGCCAGTTTGTGGAACCT 300
 Db 314 TTATAGAAGAGCTGTGCGGTCTGTAAAGAAACGCTTAAACGCCAGTTTGTGGAACCT 373
 QY 301 GCAAGGGGTAAATTACGGGCTGACACTTCAGGAGCACAGATGTGTGGAATCGAACCA 360
 Db 374 GCAAGGGGTAAATTACGGGCTGACACTTCAGGAGCACAGATGTGTGGAATCGAACCA 433
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 Db 434 CCCACTTTTGGAAATGATTCTCAAGATCATTCATCAGAGGACCAACACAGTGCCCTTTG 493
 QY 421 ACCTGGTGTCCCAACGAGGATGGCGATGTGGCTGTGGAGTTCACCCCTCGATTCACTTCA 480
 Db 494 ACCTGGTGTCCCAACGAGGATGGCGATGTGGCTGTGGAGTTCACCCCTCGATTCACTTCA 553
 QY 481 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCACCCCTCGATTCACTTCA 540
 Db 554 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCACCCCTCGATTCACTTCA 613
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 Db 614 CCGATGTCTATCGGCCACTACATCAGCGGTGAGGGGCCCAAGGATCCAAAGAGACCGAGG 673
 QY 601 AGATGCTGAAGGTGGGGGCCACCTCAGAGGGGTGGCGAACTGTCTTGGAACAACACT 660
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 QY 721 ACAGCTCTCTCAGAGGACGAGTCCGAGGCTCAGGCTCTGGAAGTGTGGCGTGTGTT 780
 Db 794 ACAGCTCTCTCAGAGGACGAGTCCGAGGCTCAGGCTCTGGAAGTGTGGCGTGTGTT 853
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 Db 854 TTGGCTTTGGCCATGTGCCACCTCTTCTTCAATTCCTCGGAAGCAGTATCTGAGCGGC 913
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 Db 914 AGAGCGCTCTGCGCTCAGCAGATGACGAGGAGTTCAGGACATGAGGCCAGCTGC 973
 QY 901 TGAGCCGAGCCAGCTGAGGACAGGAGTCTGAAGAGGCCCTGTGTAGTGTGTGA 960
 Db 974 TGAGCCGAGCCAGCTGAGGACAGGAGTCTGAAGAGGCCCTGTGTAGTGTGTGA 1033
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 QY 1801 TCCTGGTTTCGCCACTGGCCCTCGATTGAACCTCTGCGACCTTGGAGAGCTCGGGTGGT 1860
 Db 1874 TCCTGGTTTCGCCACTGGCCCTCGATTGAACCTCTGCGACCTTGGAGAGCTCGGGTGGT 1933
 QY 1861 CCCTGGTTTTCCTCTCGGAGAAATGAGCGCGAGAGGCTCTGCTCTGGAAGGCGCAGTG 1920
 Db 1934 CCCTGGTTTTCCTCTCGGAGAAATGAGCGCGAGAGGCTCTGCTCTGGAAGGCGCAGTG 1993
 QY 1921 TGGATGCCACTTGGCGCTAGTCTGCGCTCAGAGTCTCTTGAAGGCTGTCAAGGAA 1980
 Db 1994 TGGATGCCACTTGGCGCTAGTCTGCGCTCAGAGTCTCTTGAAGGCTGTCAAGGAA 2053
 QY 1981 AAGCAGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCCGCTG 2040
 Db 2054 AAGCAGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCCGCTG 2113
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 Db 2114 CAGCTTTGACATCTGGTGTACTCATGTGCTTCTCTTGTGTACCCCTCTCCAGTATT 2173
 QY 2101 ACCATTGGCCCTCAGCTGCCCTTGGTGGCTTTTAGTGCAAGACAGATGGGGCTGTTT 2160
 Db 2174 ACCATTGGCCCTCAGCTGCCCTTGGTGGCTTTTAGTGCAAGACAGATGGGGCTGTTT 2233
 QY 2161 TCCCGCCACCTCTGAGTAGTTGGAGGTCAACATACAGCTCTTTTATTTATGGCTTTTCT 2220
 Db 2234 TCCCGCCACCTCTGAGTAGTTGGAGGTCAACATACAGCTCTTTTATTTATTTGCTTTTCT 2293
 QY 2221 GCCTCTGAATGTTTCATCTCTGCTCTCTTTTGTGAGGGCGAGGAGGGTGCCTCAGGG 2280

1862 TCCTGTTTCGCCACTGGCCCTGATTTGAACTCTCTGCACCTTGGAGAGAGCTCGGGTGGT 1921
1861 CCCTGTTTTCCTCTCGAGAGATGAGCGCGAGAGGCTCGCCTCTCTGAAGGACCGAGTG 1920
1922 CCCTGTTTTCCTCTCGAGAGATGAGCGCGAGAGGCTCGCCTCTCTGAAGGACCGAGTG 1981
1921 TGGATGCACCTGGCTAGTGTCTTGGCTTCAAGCTTCTTGGAGAGCTGTCAAGGAA 1980
1982 TGGATGCACCTGGCTAGTGTCTTGGCTTCAAGCTTCTTGGAGAGCTGTCAAGGAA 2041
1981 AAGCAGCGGCTGGCAGCCTGAGCATATGCGCTCTTGGGCTCCCTCATCCAGCCGCTCG 2040
2042 AAGCAGCGGCTGGCAGCCTGAGCATATGCGCTCTTGGGCTCCCTCATCCAGCCGCTCG 2101
2041 CAGCTTTGACATCTTGGTGTACTCATGTGCGCTCTCTCTGTGTGTATACCCCTCCCAAGTAT 2100
2102 CAGCTTTGACATCTTGGTGTACTCATGTGCGCTCTCTCTGTGTGTATACCCCTCCCAAGTAT 2161
2101 ACCATTTGCCCTCACCCTGGCTTGGTGAAGCTTTTGTGCAAGACAGATGGGGCTGTTT 2160
2162 ACCATTTGCCCTCACCCTGGCTTGGTGAAGCTTTTGTGCAAGACAGATGGGGCTGTTT 2221
2161 TCCCCCACTCTGAGTAGTGGAGTGCATACACAGCTCTTTTATTTGTCCTTTTCT 2220
2222 TCCCCCACTCTGAGTAGTGGAGTGCATACACAGCTCTTTTATTTGTCCTTTTCT 2281
2221 GCCTCTGAATGTTTCACTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280
2282 GCCTCTGAATGTTTCACTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2341
2281 GCCGACCTAGTATGATGAGTGTCCAGTGTGAAAGAGAGAAATTTAAACATGTTGCAACC 2340
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RESULT 6

US-10-617-217A-76
; Sequence 76, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 2401
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (103)..(1158)
US-10-617-217A-76

Query Match 99.2%; Score 2336.8; DB 16; Length 2401;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 ATCCTTGGCGCCACAGTCGGCCACCGGGCTCGCGCGCTCATGAGAGAGCGAGGCGGC 60

QY

782 ACAGCTTGTCTGACAGGCGAGAGTCGAGCGTCAGGCTCTGGAAGTGTCTGCGCTGGTTT 841
781 TTGGCTTTGCCACATGTGCCACCTCTCTCTTCTTCTCCGGAAGCAGATATCTGACGGCG 840
842 TTGGCTTTGCCACATGTGCCACCTCTCTCTTCTTCTTCTCCGGAAGCAGATATCTGACGGCG 901
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902 AGGAGCGCTCGGCTCAAGCAGATGCAAGAGGAGTTCAGGAGCATGAGCCAGCTGCG 961
901 TGAGCCGAGCAAGCCTGAGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 960
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1081 TACCCCTGTACAAAGCTAATAGTTTGGAGCGGCACAGCTTGACTGGAAGCACCCTG 1140
1142 TACCCCTGTACAAAGCTAATAGTTTGGAGCGGCACAGCTTGACTGGAAGCACCCTG 1201
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1321 GCCTCACCCTGGAGAGTCCGCTGCTCTCTCCAGGAGCCAGATCAGTGCAGTGTG 1380
1382 GCCTCACCCTGGAGAGTCCGCTGCTCTCTCCAGGAGCCAGATCAGTGCAGTGTG 1441
1381 ACTGAAAATGCCCTCATCACTTAAGCAACAAAGCAGTGTATCAGAGCTCTTCTGTCCTG 1440
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1502 TGTCTTCTGTTTTTCTGCTGATCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1561
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1622 CTGCGCAGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1681
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1802 CGGGGCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGAGCTTGGTTCAGCAGGCC 1861
1801 TCCTGGTTTCGCCACTGCGCCCTGATTTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860

QY

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Qy
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Db 122 CCTCGCTGTGCCAGTTTCATCTCTGGGACACCTCTGTGGTCAACCGCGCCCTGTACT 181
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Db 182 CCGTGTACCGCAGAGCGCCGGGTCTCCCAAGAGCTCAAGGAGCTTAAAGAAAGTTCAAT 241
Qy 181 TGGGTCAAGATTTAAAGAGTATCTTTCAAGAGCTCAAGAAATCGTGTACTGCTG 240
Db 242 TGGGTCAAGATTTAAAGAGTATCTTTCAAGAGCTCAAGAAATCGTGTACTGCTG 301
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Qy 421 ACCTGGTGCCTCAGGAGATGCGGTGATGTCGCTGGGTGAGTGTGGAATCGAACCA 480
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Db 722 CTGTCCGCTTCAGCGCCCAACCAAGGATGAGTATCATCTAAGCAGCAGAGCTTCG 781
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Db 782 ACAGCTGCTCAGAGGAGAGTGCAGCTCAGCTCTGAAAGTGTGCGCTGCTGTT 841
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Db 842 TTGGCTTTGCCACATGTGCCACCTCTCTTCATCTCCGAAAGCAGTATCTGAGCGGC 901
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Db 902 AGAGCGCCTTCGCTCAAGCAGATGAGGAGAGTGTGAAGAGCGCTGTGTAGTGTCTGA 961
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Db 1022 GCAGCTTCAAGTCTCTGCTCTTTCTGGAGTGGGACAGTGTGTTCTCTGACCGAGTCT 1081
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Db 1082 ACCGCGCTTTCAGAGCCCAAGAGTGCCTTATCTGCACAGGCGATCACCGGGTGA 1141
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Db 1862 TCCTGGTTTCGCCACTGGCCCTGATTTGAATCTCTGCACTTGGGAGAGCTTCGGGGTGGT 1921
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Db 1982 TGGATGCACTGCGCTAGTGTCTGCGCTCACAGCTCTCTGCAAGGCTGTCTCAAGAGAA 2041
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Db 2042 AAGCAGCGGCTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCAGCCCGCTCG 2101
Qy 2041 CAGCTTTGACATCTTGGTGTACTCATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2100
Db 2102 CAGCTTTGACATCTTGGTGTACTCATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2161
Qy 2101 ACCATTTGCCCTCACCTGCGCTTGGTGTAGCTTTTGTAGTGAAGAGAGATGGGGCTGTT 2160
Db 2162 ACCATTTGCCCTCACCTGCGCTTGGTGTAGCTTTTGTAGTGAAGAGAGATGGGGCTGTT 2221
Qy 2161 TCCCCCAGCTCTGAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2220
Db 2222 TCCCCCAGCTCTGAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2281

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 1922 CCTGGTTTCCTCTCTGGAGAAATGAGGCGCAGAGGCTCGCTCTCTGAAGGAGCGAGTG 1981
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RESULT 9

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 ; Sequence 74, Application US/10042211A
 ; Publication No. US20030170719A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MATSUDA, Akio et al.
 ; TITLE OF INVENTION: NFkB Activating Gene
 ; FILE REFERENCE: 1254-0192P
 ; CURRENT APPLICATION NUMBER: US/10/042,211A
 ; CURRENT FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-402288
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP 2001-089912
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP 2001-254018
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/278,640
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/314,385
 ; NUMBER OF SEQ ID NOS: 182
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 74
 ; LENGTH: 2401
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (103)..(1158)
 ; US-10-042-211A-74

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 782 ACAGCTCTGTCAGAGGACGAGTGTGAGCTCTGAGGCTCTGAGGCTCTGAGGCTCTGAGGCT 841
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 902 AGGAGCGCTTGCCTCTCAAGCAGATGAGGAGGAGTTCAGGAGCATGAGGCGCAGCTGC 961
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 1382 GCCTCACCTGGAGGATGCGGTGGTCTCTCTCCAGGAGCAGATCAGTGGAGTGTG 1441
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 1502 TGTCT 1561
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Qy	1741	CGGGCCCCGGCACAAGATTGAAGAGAGATCATGTGAAGGCAGCTTGGTCAGGCAGGCC	1800
Db	1802	CGGGCCCCGGCACAAGATTGAAGAGAGATCATGTGAAGGCAGCTTGGTCAGGCAGGCC	1861
Qy	1801	TCTCGTTTTCGCCCATCGGCCCTGATTTGAACTCTTGCCAATTGGGAGAGACTCGGGGTGGT	1860
Db	1862	TCTCGTTTTCGCCCATCGGCCCTGATTTGAACTCTTGCCAATTGGGAGAGACTCGGGGTGGT	1921
Qy	1861	CCCTGGTTTTCCCTCTCTGAGAAATGAGGCGCAGAGCCCTCCTGAAAGACGCAGTG	1922
Db	1922	CCCTGGTTTTCCCTCTCTGAGAAATGAGGCGCAGAGCCCTCCTGAAAGACGCAGTG	1981
Qy	1921	TGGATGCCACTGSCCTFAGTGTCTCTGSCCTCACAGCTTCTTGCAAGGCTGTCAACAAGAA	1980
Db	1982	TGATGCCACTGSCCTFAGTGTCTCTGSCCTCACAGCTTCTTGCAAGGCTGTCAACAAGAA	2041
Qy	1981	AAGCAGCCGGCTGGCAACCTGAGCATATGCGCTCTTGGGGCTCCCTCATCCAGCCCGTCG	2040
Db	2042	AAGCAGCCGGCTGGCAACCTGAGCATATGCGCTCTTGGGGCTCCCTCATCCAGCCCGTCG	2101
Qy	2041	CAGCTTGACATCTTGCTGGTGACTCATGTCTCTTGTGTGTACCCCTCCCGAGTAT	2100
Db	2102	CAGCTTTGACATCTTGCTGGTGACTCATGTCTCTTGTGTGTACCCCTCCCGAGTAT	2161
Qy	2101	ACCAATTGCCCTCAGCTGCGCTTGGTGAGCCCTTTAGTGCAGAAGATGGGGCTGTTT	2160
Db	2162	ACCAATTGCCCTCAGCTGCGCTTGGTGAGCCCTTTAGTGCAGAAGATGGGGCTGTTT	2221
Qy	2161	TCGCCCACTCTGAGTAGTTGGAGGTACATACAGAGCTCTTTTATTTATTCCTTTTCT	2220
Db	2222	TCGCCCACTCTGAGTAGTTGGAGGTACATACAGAGCTCTTTTATTTATTCCTTTTCT	2281
Qy	2221	GCCTCTCAATGTTTCATCTCTCGTCTCTTTGTGCGGCGAGGAAGGGGTGCCCTCAGGG	2280
Db	2282	GCCTCTCAATGTTTCATCTCTCGTCTCTTTGTGCGGCGAGGAAGGGGTGCCCTCAGGG	2341
Qy	2281	GCCGACACTAGTATGATGCGAGTCTCAGTGTGAACAGCAGAAATTAACATGTTGCAACC	2340
Db	2342	GCCGACACTAGTATGATGCGAGTCTCAGTGTGAACAGCAGAAATTAACATGTTGCAACC	2401

	Query Match	98.9%;	Score 2330.8;	DB 9;	Length 2446;
	Best Local Similarity	99.8%;	Pred. No. 0;		
	Matches 2351;	Conservative	3;	Mismatches 0;	Indels 2;
					Gaps 2
Qy	1	ATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGTCATGTGAGAGCGAGGCGCGC	60		
Db	82	ATCCTTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGTCATGTGAGAGCGAGGCGCGC	141		
Qy	61	CCTCGCTGTGCAGTTCACTCTCTGGGCACACCTCTGTGTGTACCGCGCCCTGTACT	120		
Db	142	CCTCGCTGTGCAGTTCACTCTCTGGGCACACCTCTGTGTGTACCGCGCCCTGTACT	201		

QY 121 CCGTGTAACGGAGAGGCCCGGCTCTCCAGAGCTCAAGGAGCTTAAAGAGTTCAAT 180
DB 202 CCGTGTAACGGAGAGGCCCGGCTCTCCAGAGCTCAAGGAGCTTAAAGAGTTCAAT 261
QY 181 TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATCGTGCCCTTATGCTG 240
DB 262 TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATCGTGCCCTTATGCTG 321
QY 241 TTATAGAAGAGCTGCGGCTCTGTTTAAAGAAACGCTTAAAGCAAGTTTGTGGAATACT 300
DB 322 TTATAGAAGAGCTGCGGCTCTGTTTAAAGAAACGCTTAAAGCAAGTTTGTGGAATACT 381
QY 301 GCAAGGGGTAAATTCAGCGGCTGACATTCAGAGCACAAAGATGCTGGAATCGAACCA 360
DB 382 GCAAGGGGTAAATTCAGCGGCTGACATTCAGAGCACAAAGATGCTGGAATCGAACCA 441
QY 361 CCCACCTTTGGAATGATGCTCAAGATCATTCAGAGGACCAACACAGTGCCCTTTG 420
DB 442 CCCACCTTTGGAATGATGCTCAAGATCATTCAGAGGACCAACACAGTGCCCTTTG 501
QY 421 ACCTGCTGCCACAGAGATGCGTGGATGCTGGCTGTGGAGTGTGAAGCCCTGGACT 480
DB 502 ACCTGCTGCCACAGAGATGCGTGGATGCTGGCTGTGGAGTGTGAAGCCCTGGACT 561
QY 481 CAGTGGATCTGGGCTCTAGAGACTGTGTATGAGAACTTCCACCCCTCGATTCAAGTCTTCA 540
DB 562 CAGTGGATCTGGGCTCTAGAGACTGTGTATGAGAACTTCCACCCCTCGATTCAAGTCTTCA 621
QY 541 CCGATGTCATCGGCCACTACATACAGCGGTAGCGGCCCAAGAGACCGAGG 600
DB 622 CCGATGTCATCGGCCACTACATACAGCGGTAGCGGCCCAAGAGACCGAGG 681
QY 601 AGATGCTGAAGTGGGGCCACCTCACAGGGTGGGAACTGCTCTGAGCAACAAT 660
DB 682 AGATGCTGAAGTGGGGCCACCTCACAGGGTGGGAACTGCTCTGAGCAACAAT 741
QY 661 CTGTCGCGCTTCAGCGGCCCAAAACAGGCTGAGTACTATTAAGCAGCGCAGAGCTTCG 720
DB 742 CTGTCGCGCTTCAGCGGCCCAAAACAGGCTGAGTACTATTAAGCAGCGCAGAGCTTCG 801
QY 721 ACAGCGCTCTCAGAGGAGGAGTGAAGTCAAGCTCTGGAAGTGTGGCGTGGT 780
DB 802 ACAGCGCTCTCAGAGGAGGAGTGAAGTCAAGCTCTGGAAGTGTGGCGTGGT 861
QY 781 TTGCTTTGCCACATGTGCCACCTCTCTTCAATCTCCGGAAGCAAGTATCTGAGCGGC 840
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QY 841 AGAGCGCTCTGCGCTCAAGCAGATGAGGAGGAGTTCCAGAGCATGAGGCCAGCTGC 900
DB 922 AGAGCGCTCTGCGCTCAAGCAGATGAGGAGGAGTTCCAGAGCATGAGGCCAGCTGC 981
QY 901 TGAGCCGAGCAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 960
DB 982 TGAGCCGAGCAGCCTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA 1041
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DB 1342 TGGCAGGATGCTGCTTTTCCACCTGAGAGGGACCCCTGTCCATGTGACGCTCATCAGA 1401
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DB 1881 TCCTGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1940
QY 1861 CCCTGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
DB 1941 CCCTGTTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2000
QY 1921 TGGATGCCACTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
DB 2001 TGGATGCCACTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2060
QY 1981 AAGCAGCGGCTGGCAGCTGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
DB 2061 AAGCAGCGGCTGGCAGCTGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2120
QY 2041 CAGCTTTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
DB 2121 CAGCTTTGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2180
QY 2101 ACCATTTGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
DB 2181 ACCATTTGCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2240
QY 2161 TCCCCACCTCTGAGTAGTGGAGTCAATACAGAGCTTTTAGTGAAGACAGATGGGGCTGTTT 2220
DB 2241 TCCCCACCTCTGAGTAGTGGAGTCAATACAGAGCTTTTAGTGAAGACAGATGGGGCTGTTT 2300
QY 2221 GCCTCTGAATGTTTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
DB 2301 GCCTCTGAATGTTTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2359
QY 2281 GCGCACACTAGTATGATGAGTGTCCAGTGTGAACAGACAGAAATTAACAATGTGCAACC 2340

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2004, 20:08:22 ; Search time 1047 Seconds
(without alignments)
11812.451 Million cell updates/sec

Title: US-09-978-360A-32

Perfect score: 2356

Sequence: 1 atcctggcgccacagtcgg.....aaccaaaaaaaaaaaaaa 2356

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2356	100.0	2356	3	AA87756 Human sec
2	2356	100.0	2356	5	AA64038 cDNA enco
3	2356	100.0	2356	12	ADP18776 Human sec
4	2338.4	99.3	2413	4	AD12597 Human pro
5	2336.8	99.2	2401	6	ABQ91949 Human NF-
6	2335.2	99.1	2401	6	ABQ91948 Human NF-
7	2332	99.0	2442	4	AAH16130 Human cDN
8	2330.8	98.9	2431	4	AA502044 DNA enco
9	2330.8	98.9	2446	4	AA525835 Human cDN
10	2330.8	98.9	2446	8	ABX73176 Human nov
11	2291.8	97.3	2717	6	ABN59817 Novel hum
12	2217	94.1	2377	5	ABA82998 Human tra
13	1907.4	81.0	2080	8	ABT42547 Human nuc
14	1766	75.0	1791	4	AA526296 Human nov
15	1766	75.0	1791	8	ABX73637 Human nov
16	1751.4	74.3	1780	6	ABL90713 Human pol
17	476.6	20.2	512	4	AAH11159 Human cDN
18	435	18.5	435	10	AA59606 Human gen
19	363	15.4	374	6	ABL66011 Lung canc
20	338.8	14.4	484	4	AAH06088 Human cDN
21	309	13.1	343	2	AA51937 Human sec

22	307.4	13.0	378	2	AA40363 Human sec
23	304.6	12.9	391	2	AA40593 Human sec
24	290.8	12.3	398	8	ABX5547 Bovine ES
25	124.6	5.3	197	2	AA40327 Human sec
26	95.6	4.1	1086	4	ABL2113 Drosophil
27	74.6	3.2	3475	4	ABL2112 Drosophil
28	65.2	2.8	5019	4	ABL26430 Drosophil
29	60.6	2.6	4086	4	ABL2110 Drosophil
30	60	2.5	60	6	ABN40374 Human spl
31	58.6	2.5	2000	8	ADA71938 Rice gene
32	53.4	2.3	2000	8	ADA71938 Rice gene
33	51	2.2	51	4	AAI78808 Human sil
34	49.4	2.1	51	4	AAI78809 Human sil
35	45.8	1.9	1239	9	ACF06126 Bacterial
36	45.8	1.9	4356	2	AAQ37543 Cardiac a
37	45.6	1.9	4161	4	ABL09363 Drosophil
38	45.6	1.9	24066	4	ABL09362 Drosophil
39	45.4	1.9	412	8	ABX54826 Bovine ES
40	44.8	1.9	5120	4	AA84677 DNA seque
41	44.8	1.9	5285	12	ADL23241 Mutant hu
42	44.2	1.9	4356	2	AAQ95540 Cardiac a
43	43.2	1.8	1227	2	AAV84121 Pentactet
44	42.8	1.8	1716	12	ADJ40227 Plant cDN
45	42.8	1.8	1782	8	ADA71107 Rice gene

ALIGNMENTS

RESULT 1
AA87756
ID AAA87756 standard; cDNA; 2356 BP.
AC AAA87756;
XX
DT 28-NOV-2000 (first entry)
XX
DE Human secreted protein encoding cDNA SEQ ID #55.
XX

Human; secreted protein; forensic procedure; gene therapy;
chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
brain disorder; skeletal muscle disorder; eye disorder; obesity;
mitochondriopathy; diabetes; atherosclerosis; Alzheimer's disease;
neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
septic shock; impotence; ss.
Homo sapiens.

WO200037491-A2.
XX
PD 29-JUN-2000.
XX
PF 20-DEC-1999; 99WO-IB002058.
XX
PR 22-DEC-1998; 99US-0113686P.
XX
PR 25-JUN-1999; 99US-0141032P.
XX
PA (GBST) GENSET.
XX
XX Bougueleret L, Dumas J, Duclert A;
XX WPI; 2000-442637/38.
XX P-PSDB; AAB25794.
XX
XX Polynucleotides and polypeptides encoding proteins with signal peptides,
XX useful in diagnostic, forensic, gene therapy and chromosome mapping
XX procedures.
XX Claim 1; Page 218-220; 306pp; English.

This sequence represents human cDNA encoding a secreted protein. The
invention relates to sequences AAA87725-A87774 which encode human

secreted proteins AAB25763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene therapy and chromosome mapping procedures and may be used to design expression vectors and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis, neurodegenerative disorders, graft rejection, Alzheimer's disease, dementia, hyperlipidemia, septic shock and impotence

XX
SQ Sequence 2356 BP; 494 A; 651 C; 665 G; 546 T; 0 U; 0 Other;

Query Match 100.0%; Score 2356; DB 3; Length 2356;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCTTTGGCGCCACAGTCGGCCACCGGGGCTGCGCCCGTCTATGGAGCGGAGCGCGC 60
Db 1 ATCTTTGGCGCCACAGTCGGCCACCGGGGCTGCGCCCGTCTATGGAGCGGAGCGCGC 60

QY 61 CTCTGCTGTCGAGTTTCATCTCTCTGGGACCACTCTGTGGTCAAGCGCGCCCTTACT 120
Db 61 CTCTGCTGTCGAGTTTCATCTCTCTGGGACCACTCTGTGGTCAAGCGCGCCCTTACT 120

QY 121 CCGGTACCGGCAAGAGGCGCGGCTCTCCAGAGCTCAAGGAGCTAAAGAGTTCAAT 180
Db 121 CCGGTACCGGCAAGAGGCGCGGCTCTCCAGAGCTCAAGGAGCTAAAGAGTTCAAT 180

QY 181 TGGGTGAAGATTTAAGAGTATTTTTCAGAACTCCAGAAATCGTGCCCTTATGCTG 240
Db 181 TGGGTGAAGATTTAAGAGTATTTTTCAGAACTCCAGAAATCGTGCCCTTATGCTG 240

QY 241 TTATAGAAGAGCTGTGCGGTGTTTAAAGAAAGCTTAAAGAGCTTGTGGAAGACT 300
Db 241 TTATAGAAGAGCTGTGCGGTGTTTAAAGAAAGCTTAAAGAGCTTGTGGAAGACT 300

QY 301 GCAAGGGGGTAAATTCAGCGGCTGACACTTCAGAGCAACAAGATGGTGAATCGAACCA 360
Db 301 GCAAGGGGGTAAATTCAGCGGCTGACACTTCAGAGCAACAAGATGGTGAATCGAACCA 360

QY 361 CCCACCTTTGGAATGATGCTCAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG 420
Db 361 CCCACCTTTGGAATGATGCTCAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG 420

QY 421 ACCTGGTGGCCACAGAGTGGCTGATGGCTGCGAGTCTGAAGCCCTGGACT 480
Db 421 ACCTGGTGGCCACAGAGTGGCTGATGGCTGCGAGTCTGAAGCCCTGGACT 480

QY 481 CAGTGGATCTGGGCTTAGAGACTGTGTATGAGAAAGTTCCACCCCTGATTCAGTCTTCA 540
Db 481 CAGTGGATCTGGGCTTAGAGACTGTGTATGAGAAAGTTCCACCCCTGATTCAGTCTTCA 540

QY 541 CCGATGTCATCGGCGCATATCATCAGCGTGAAGCGGCGCAAGGCGATCCAGAGACCGAGG 600
Db 541 CCGATGTCATCGGCGCATATCATCAGCGTGAAGCGGCGCAAGGCGATCCAGAGACCGAGG 600

QY 601 AGATGCTGAAGTGGGGCCACCTCTCAAGGGGTTGGCGAACTGCTCTGGACCAACT 660
Db 601 AGATGCTGAAGTGGGGCCACCTCTCAAGGGGTTGGCGAACTGCTCTGGACCAACT 660

QY 661 CTGTCCGCTTCAGCGCGCCAAACAAAGGATGCGAGTACTATCTAAGCAGCAGGACTTCG 720
Db 661 CTGTCCGCTTCAGCGCGCCAAACAAAGGATGCGAGTACTATCTAAGCAGCAGGACTTCG 720

QY 721 ACAGCTGCTGCAGAGGCGAGGAGTCAGCGTCAGGCTCTGGAAGGTCGTGGCGCTGGTTT 780

Db 721 ACAGCTGCTGCAGAGGCGAGGTCAGCGTCAGGCTCTGGAAGGTCGTGGCGCTGGTTT 780
QY 781 TTGGCTTTGCCACATGTGCGCACCTCTTCTTCTCCGGAAGCAGTATCTGACGCGC 840
Db 781 TTGGCTTTGCCACATGTGCGCACCTCTTCTTCTCCGGAAGCAGTATCTGACGCGC 840

QY 841 AGGAGCGCTCGCTCAAGCAGATGACAGGAGTTCAGAGGAGTTCAGAGCATGAGGCCAGCTGC 900
Db 841 AGGAGCGCTCGCTCAAGCAGATGACAGGAGTTCAGAGGAGTTCAGAGCATGAGGCCAGCTGC 900

QY 901 TGAGCCGAGCCAAAGCTTCAGACAGGAGTCTGAAGAGCGCTGTGTAGTGTCTTGA 960
Db 901 TGAGCCGAGCCAAAGCTTCAGACAGGAGTCTGAAGAGCGCTGTGTAGTGTCTTGA 960

QY 961 GAGCTTCAAGTCTCGCTCTTCTTCTGAGTGGGACAGTGTGCTTCTGACCGAGTGT 1020
Db 961 GAGCTTCAAGTCTCGCTCTTCTTCTGAGTGGGACAGTGTGCTTCTGACCGAGTGT 1020

QY 1021 ACCGCGCTTGCAGAGCGCCAAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGGTGA 1080
Db 1021 ACCGCGCTTGCAGAGCGCCAAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGGTGA 1080

QY 1081 TACCCCTGTACAAAGCTAATAGTTTGAAGCGGACAGCTTGACTGAGAGCACCCCTG 1140
Db 1081 TACCCCTGTACAAAGCTAATAGTTTGAAGCGGACAGCTTGACTGAGAGCACCCCTG 1140

QY 1141 CCGCTTTTCAGGATTTTATCTCAGGCGCTTTCAGGAGCAGTGGTGGGGTAGCTGT 1200
Db 1141 CCGCTTTTCAGGATTTTATCTCAGGCGCTTTCAGGAGCAGTGGTGGGGTAGCTGT 1200

QY 1201 CACTCCAGGTATGATTGAGGAGGAAATGGGTAGAAACTCTCCAGACCATGCTCCCAA 1260
Db 1201 CACTCCAGGTATGATTGAGGAGGAAATGGGTAGAAACTCTCCAGACCATGCTCCCAA 1260

QY 1261 TGGCAGATGCTGCTTCCACCTCAGAGGAGACCTGTCCATGTGAGCCTCATCAGA 1320
Db 1261 TGGCAGATGCTGCTTCCACCTCAGAGGAGACCTGTCCATGTGAGCCTCATCAGA 1320

QY 1321 GCTCACCTCGGAGATGCGGTGGGTCTCTCCAGAGGAGGAGTCAAGTGGAGTGTG 1380
Db 1321 GCTCACCTCGGAGATGCGGTGGGTCTCTCCAGAGGAGGAGTCAAGTGGAGTGTG 1380

QY 1381 ACTGAAATGCTCTCATCATTAAGCACCAAGCAGTGTAGCAGCTCTTCTGTCCTG 1440
Db 1381 ACTGAAATGCTCTCATCATTAAGCACCAAGCAGTGTAGCAGCTCTTCTGTCCTG 1440

QY 1441 TGTCTTCTGTTTTTCTGTTGTAATCGTTGCTGTGAGTGTGGAGTGTGAGTCTCAG 1500
Db 1441 TGTCTTCTGTTTTTCTGTTGTAATCGTTGCTGTGAGTGTGGAGTGTGAGTCTCAG 1500

QY 1501 GGGAGGAAAGCTGGGCGGCGGAGTACAAAGGAGTGGGTGCTGCTCCGAGAGACT 1560
Db 1501 GGGAGGAAAGCTGGGCGGCGGAGTACAAAGGAGTGGGTGCTGCTCCGAGAGACT 1560

QY 1561 CTGCGCAGCTTTTCTTCTTTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAAATGT 1620
Db 1561 CTGCGCAGCTTTTCTTCTTTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAAATGT 1620

QY 1621 CAGCTGGGAGGTCAGCTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680
Db 1621 CAGCTGGGAGGTCAGCTTGTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680

QY 1681 CAGCTGTGTGTAGAGGACAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740
Db 1681 CAGCTGTGTGTAGAGGACAAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1740

QY 1741 CCGGCGCGCGCGGCAACAGATTTGAAGAGAGATCATGTGAAGGCGAGTGGTCAGGACGCC 1800
Db 1741 CCGGCGCGCGCGGCAACAGATTTGAAGAGAGATCATGTGAAGGCGAGTGGTCAGGACGCC 1800

QY 1801 TCCTGGTTTCCCACTGGCCCTGATTTGAACTCTCTGCCACTTTGGGAGAGCTCGGGGTGT 1860

Db 1801 TCCTGTTTGGCCACTGGCCCTGATTGAACTCCTGCCACTTGGGAGAGCTGGGGTGT 1860
 QY CCTGCTTTTCCCTCCTGGAGATGAGCGCAGAGGCTCGCTCCTCTGAAGGACGAGTG 1920
 Db CCTGCTTTTCCCTCCTGGAGATGAGCGCAGAGGCTCGCTCCTCTGAAGGACGAGTG 1920
 QY TGGATGCCACTGCGCTAGTGTCTCTGGCCCTCACAGCTTCCCTGCAAGGCTGTCAACAGGAA 1980
 Db TGGATGCCACTGCGCTAGTGTCTCTGGCCCTCACAGCTTCCCTGCAAGGCTGTCAACAGGAA 1980
 QY 1981 AAGCAGCGGCTGGACCTGAGCATATGCCCCCTTGGGGCTCCCTCATCCAGCCCGTGG 2040
 Db 1981 AAGCAGCGGCTGGACCTGAGCATATGCCCCCTTGGGGCTCCCTCATCCAGCCCGTGG 2040
 QY 2041 CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTTGTGTGTGTGTGTGTGTGTGTGT 2100
 Db 2041 CAGCTTTGACATCTTGGTGTACTCATGTGCTTCTCTTGTGTGTGTGTGTGTGTGTGTGT 2100
 QY 2101 ACCATTGCCCCCTACCTGCCCCCTTGGTGGAGCTTGTGAGCCCTTTTGTGCAAGACAGATGGGGCTGTTT 2160
 Db 2101 ACCATTGCCCCCTACCTGCCCCCTTGGTGGAGCTTGTGAGCCCTTTTGTGCAAGACAGATGGGGCTGTTT 2160
 QY 2161 TCCCCCACTCTGAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2220
 Db 2161 TCCCCCACTCTGAGTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 2220
 QY 2221 GCCTCTGAATGTTTCACTCTGCT 2280
 Db 2221 GCCTCTGAATGTTTCACTCTGCT 2280
 QY 2281 GCGGACACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 Db 2281 GCGGACACTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340
 QY 2341 AAAAAAAAAAAAAA 2356
 Db 2341 AAAAAAAAAAAAAA 2356

RESULT 2

AAF64038
 ID AAF64038 standard; cDNA; 2356 BP.
 XX AC AAF64038;
 XX DT 05-APR-2001 (first entry)
 XX DE cDNA encoding human secreted protein #39.
 XX KW Secreted protein; prevention; treatment; diagnosis; disease; infection;
 XX OS ds.
 XX OS Homo sapiens.
 XX PN WO200100806-A2.
 XX PD 04-JAN-2001.
 XX 21-JUN-2000; 2000WO-IB0000951.
 XX PF 25-JUN-1999; 99US-0141032P.
 XX PR 21-DEC-1999; 99US-00469099.
 XX (GIST) GENSET.
 XX Dumas Milne Edwards J, Bougueleret L, Jobert S;
 XX WPI; 2001-071487/08.
 XX 49 Secreted proteins and the nucleic acids encoding them, useful in gene
 XX therapy and for detecting similar sequences in samples.
 XX Claim 1; Page 257-258; 307pp; English.

XX The present invention relates to 49 Secreted proteins and the cDNAs
 CC encoding them. The protein and nucleic acids may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate protein expression
 XX Sequence 2356 BP; 494 A; 651 C; 665 G; 546 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2356; DB 5; Length 2356;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATCTTGGCGCCACAGTGGCCACCGGGCTCGCCGCTCATGGAGAGCGAGGCGGC 60
 Db 1 ATCTTGGCGCCACAGTGGCCACCGGGCTCGCCGCTCATGGAGAGCGAGGCGGC 60
 QY 61 CCTCGCTGTGCCAGTTCATCTCTTGGGCAACCTCTGTGTGTCACCGCCCTGTACT 120
 Db 61 CCTCGCTGTGCCAGTTCATCTCTTGGGCAACCTCTGTGTGTCACCGCCCTGTACT 120
 QY 121 CCGTGTACCGGAGAGGCGCGGCTCTCCAGAGCTCAAGGAGCTAAAAAGTTCAAT 180
 Db 121 CCGTGTACCGGAGAGGCGCGGCTCTCCAGAGCTCAAGGAGCTAAAAAGTTCAAT 180
 QY 181 TGGGTGAAGATTAAAGAGTATTTTTCAGAGCTCCAGGAAATGCGTTCATGCTG 240
 Db 181 TGGGTGAAGATTAAAGAGTATTTTTCAGAGCTCCAGGAAATGCGTTCATGCTG 240
 QY 241 TTATAGAGGAGCTGTGGCTGTGTTAAAGAAACGCTTAAAGCAGTTTGTGAAAACT 300
 Db 241 TTATAGAGGAGCTGTGGCTGTGTTAAAGAAACGCTTAAAGCAGTTTGTGAAAACT 300
 QY 301 GCAAGGGGTAATTTCAGCGGTGACACTTCAGGAGCACAAGATGCTGGAATCGAAC 360
 Db 301 GCAAGGGGTAATTTCAGCGGTGACACTTCAGGAGCACAAGATGCTGGAATCGAAC 360
 QY 361 CCCACCTTTGGAATGATTGCTCAAAGATCAATTCATCAGAGCACAACACAGTGCCTTTG 420
 Db 361 CCCACCTTTGGAATGATTGCTCAAAGATCAATTCATCAGAGCACAACACAGTGCCTTTG 420
 QY 421 ACCTGTGCCCCCAGAGATGGCGTGGATGCTGCGAGTGTGAAGCCCTTGGACT 480
 Db 421 ACCTGTGCCCCCAGAGATGGCGTGGATGCTGCGAGTGTGAAGCCCTTGGACT 480
 QY 481 CAGTGAATCTGGGTCTAGAGACTGTGTATGAGAGTTCCACCCCTCGATTGCTCTCA 540
 Db 481 CAGTGAATCTGGGTCTAGAGACTGTGTATGAGAGTTCCACCCCTCGATTGCTCTCA 540
 QY 541 CCGATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCATCCAGAGACCGAGG 600
 Db 541 CCGATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGCATCCAGAGACCGAGG 600
 QY 601 AGATGCTGAAGGTGGGGCCACCTTCACAGGGTTGGCGAACTGGTCTTGACAACT 660
 Db 601 AGATGCTGAAGGTGGGGCCACCTTCACAGGGTTGGCGAACTGGTCTTGACAACT 660
 QY 661 CTGTCCGCTGTCAGCGCCCAACAGGATGAGTACTATCTAAGCAGCAGGACTTCG 720
 Db 661 CTGTCCGCTGTCAGCGCCCAACAGGATGAGTACTATCTAAGCAGCAGGACTTCG 720
 QY 721 ACAGCTGTGTCAGAGCAGGAGTTCAGCGCTCAGGCTCTGGAAGGTCTCGCGCTGTT 780
 Db 721 ACAGCTGTGTCAGAGCAGGAGTTCAGCGCTCAGGCTCTGGAAGGTCTCGCGCTGTT 780
 QY 781 TTGGCTTTGCCCATGTGCCACCTCTTCTTCAATTCGGAAGAGTATCTCAGCGGC 840
 Db 781 TTGGCTTTGCCCATGTGCCACCTCTTCTTCAATTCGGAAGAGTATCTCAGCGGC 840
 QY 841 AGGAGCGCTGCGCTCAAGCAGATGAGGAGTTCAGGAGCAGTGGCCAGCTGC 900
 Db 841 AGGAGCGCTGCGCTCAAGCAGATGAGGAGTTCAGGAGCAGTGGCCAGCTGC 900
 QY 901 TGAGCGAGCCAAAGCCTTGAGGAGCAGGAGTCTGGAAGCGCTGTGTAGTGTGCTGA 960

D _b	901	TGAGCCGCAGCAAGCCTGGAGACAGGAGAGTCTGAAGAGCGCCTGTGTAGTGTCGTGA	960
Q _y	961	GCAGCTTCAAGTCTCTCGCTCTTTCTGGAGTGTGGCACGTTTGTTCCTGCAACCAGTGCT	1020
D _b	961	GCAGCTTCAAGTCTCTCGCTCTTTCTGGAGTGTGGCACGTTTGTTCCTGCAACCAGTGCT	1020
Q _y	1021	ACCGCGCTTTGCCAGAGCCCCAGAAGTGCCTATCTGCAGACAGCGCATCACCCGGGTGA	1080
D _b	1021	ACCGCGCTTTGCCAGAGCCCCAGAAGTGCCTATCTGCAGACAGCGCATCACCCGGGTGA	1080
Q _y	1081	TACCCCTGTACACACTAATAGTTTGGAAAGCGGCACAGCTTGACTCGAAAGCACCCCCTG	1140
D _b	1081	TACCCCTGTACACACTAATAGTTTGGAAAGCGGCACAGCTTGACTCGAAAGCACCCCCTG	1140
Q _y	1141	CCCCCTTTTCAGGGATTTTTTATCTCGAGGCGCTTTGAGAGAGCAGTGGTGGGGTAGCTGT	1200
D _b	1141	CCCCCTTTTCAGGGATTTTTTATCTCGAGGCGCTTTGAGAGAGCAGTGGTGGGGTAGCTGT	1200
Q _y	1201	CACCTCCAGGTATGATTGAGGGAGGAATTGGGTAGAACTCTCCAGACCCATGCCCTCAA	1260
D _b	1201	CACCTCCAGGTATGATTGAGGGAGGAATTGGGTAGAACTCTCCAGACCCATGCCCTCAA	1260
Q _y	1261	TGGCAGAGATGCTGCTTTCCCACTGAGAGGGAGCCCTGTCATGTGCAGCCTCATCAGA	1320
D _b	1261	TGGCAGAGATGCTGCTTTCCCACTGAGAGGGAGCCCTGTCATGTGCAGCCTCATCAGA	1320
Q _y	1321	GCTTCACCCCTGGGAGGATGCCGTGGCGTCTCTCCAGGAGCGAGATCAGTCGAGTG TG	1380
D _b	1321	GCTTCACCCCTGGGAGGATGCCGTGGCGTCTCTCCAGGAGCGAGATCAGTCGAGTG TG	1380
Q _y	1381	ACTGAAATAGCTCATCATTAGACACAAGCGAGTGATCAGCAGCTCTCTGTTCCTG	1440
D _b	1381	ACTGAAAAATGCTCATCATTAGACACAAGCGAGTGATCAGCAGCTCTCTGTTCCTG	1440
Q _y	1441	TGCTCTCTGTTTTTTTCTCTGGTGAATCGTGTGCTGTGGACATCAGCAGCTCTTCTGTTCC TG	1500
D _b	1441	TGCTCTCTGTTTTTTTCTCTGGTGAATCGTGTGCTGTGGACATCAGCAGCTCTTCTGTTCC TG	1500
Q _y	1501	GGGAGGAAAAGCTGGGCCCCGAGTACAACGAGATGCCCTTGGGTGCTGCTCCGAGAGACT	1560
D _b	1501	GGGAGGAAAAGCTGGGCCCCGAGTACAACGAGATGCCCTTGGGTGCTGCTCCGAGAGACT	1560
Q _y	1561	CTGGCGCAGCTTTCTTCTTTTCTCATGCCCGGGAACAGTCTTTCTTCAGAAATG GT	1620
D _b	1561	CTGGCGCAGCTTTCTTCTTTTCTCATGCCCGGGAACAGTCTTTCTTCAGAAATG GT	1620
Q _y	1621	CAGGCTGGGCAGGTCAA CTGTGTGTTCTTTTCCCTCACTGCTTGCTCTTAACCGCTG	1680
D _b	1621	CAGGCTGGGCAGGTCAA CTGTGTGTTCTTTTCCCTCACTGCTTGCTCTTAACCGCTG	1680
Q _y	1681	CACGTGTGTAGAGAACAAAGAAAGTGAAGTCAAGAGATCATGTGAAGGCGAGTTGGTCA	1740
D _b	1681	CACGTGTGTGTAGAGAACAAAGAAAGTGAAGTCAAGAGATCATGTGAAGGCGAGTTGGTCA	1740
Q _y	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGGTCAAGGCGCC	1800
D _b	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCGAGTTGGTCAAGGCGCC	1800
Q _y	1801	TCTGTGTTTTCGGCACTGGCCCTGATTGAACTCTCTGCACTTGGAGAGCTCGGGGTGGT	1860
D _b	1801	TCTGTGTTTTCGGCACTGGCCCTGATTGAACTCTCTGCACTTGGAGAGCTCGGGGTGGT	1860
Q _y	1861	CCCTGGTTTTCCCTCTCTGAGAAATGAGGCGCAGAGCCTCGCTCTTCAGAGGACGCA GTG	1920
D _b	1861	CCCTGGTTTTCCCTCTCTGAGAAATGAGGCGCAGAGCCTCGCTCTTCAGAGGACGCA GTG	1920
Q _y	1921	TGGATGCACATGGCCTAGTGTCTGGCCTTCAGAGCTTCTTTCGCAAGGCTGTCAAGGAA	1980
D _b	1921	TGGATGCACATGGCCTAGTGTCTGGCCTTCAGAGCTTCTTTCGCAAGGCTGTCAAGGAA	1980
Q _y	1981	AAGCAGCGCGCTGGCAACCTTGAGCATATGCCCTCTTTGGGGCTCCCTCATCCAGGCCGTG	2040

Db	1981	AAAGCAGCCGGCTGGCACCCCTGAGCATATAGCCCTCTTTGGGGCTCCCTCATCCAGCCGCTCG	2040
QY	2041	CAGCTTTGACATCTTGGTGTACTCATGTGCGCTTCTCCTTTGTGTATACCCCTCCAGTATT	2100
Db	2041	CAGCTTTGACATCTTGGTGTACTCATGTGCGCTTCTCCTTTGTGTATACCCCTCCAGTATT	2100
QY	2101	ACCATTGGCCCTCACCTGCCCTTGTGTAGCCTTTTAGTGCAGAAGATGGGCTGTTT	2160
Db	2101	ACCATTGGCCCTCACCTGCCCTTGTGTAGCCTTTTAGTGCAGAAGATGGGCTGTTT	2160
QY	2161	TCCCCACCTCTGAGTAGTTGGAGTGCATACACAGCTCTTTTATTTGCCCCCTTTCT	2220
Db	2161	TCCCCACCTCTGAGTAGTTGGAGTGCATACACAGCTCTTTTATTTGCCCCCTTTCT	2220
QY	2221	GCCTCTGAATGTTTCATCTCTCGTCCTTCTTGTGCGAGGCGAGGAAGGGTGCCTCAGGG	2280
Db	2221	GCCTCTGAATGTTTCATCTCTCGTCCTTCTTGTGCGAGGCGAGGAAGGGTGCCTCAGGG	2280
QY	2281	GCGGACACTAGTAGTATGATGCGAGTCCAGTGTGAACAGCAGAAATTAAACATGTTGCNAAC	2340
Db	2281	GCGGACACTAGTAGTATGATGCGAGTCCAGTGTGAACAGCAGAAATTAAACATGTTGCNAAC	2340
QY	2341	AAAAAATAAAAAAAAAA 2356	
Db	2341	AAAAAATAAAAAAAAAA 2356	
RESULT 3			
ADP18776	ADP18776 standard; cDNA; 2356 BP.		
ID			
XX	ADP18776;		
XX			
DT	26-AUG-2004 (first entry)		
XX			
DE	Human secreted polynucleotide #32.		
XX			
KW	Human; secreted protein; gene; ss; genetic disease.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004110939-A1.		
XX			
PD	10-JUN-2004.		
XX			
PF	15-OCT-2001; 2001US-00978360.		
XX			
PR	17-DEC-1998; 98WO-IB002122.		
PR	09-FEB-1999; 99WO-IB000282.		
PR	21-JUN-2000; 2000WO-IB000951.		
PR	15-SEP-2000; 2000US-00663600.		
XX			
XX	(GEST) GENSET SA.		
PA			
XX			
PI	Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;		
PI	Duclert A;		
XX			
DR	WPI; 2004-440404/41.		
DR	P-PSDB; ADP19181.		
PT	New isolated polynucleotide encoding secreted polypeptide, useful for		
PT	gene therapy, or in diagnostic procedures to identify individuals having		
PT	genetic diseases resulting from abnormal expression of the genes.		
XX			
PS	Claim 1; SEQ ID NO 32; 113pp; English.		
XX			
CC	The invention relates to human cDNA sequences that encode human secreted		
CC	proteins. The invention also relates to an antibody that specifically		
CC	binds to a polypeptide of the invention and a method of binding the		
CC	polypeptide to an antibody. The polynucleotides are useful for expressing		
CC	the entire secreted proteins which they encode and for distinguishing		
CC	human tissues and cells from non-human tissues and cells, and for		
CC	distinguishing between human tissues and cells that do or do not express		

the polynucleotides comprising the cDNAs. The polynucleotides and polypeptides are useful in forensic procedures or diagnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence represents a human secreted polynucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

[illegible]

QY	541	CCGATGTCATCGCGCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACCGAGG	600
DB	614	CCGATGTCATCGGCGCACTATCATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACCGAGG	673
QY	601	AGATGCTGAAGGTGGGGCCACCCTCACAGGGTTTGGCGAACTGCTCTCGACCAACAACCT	660
DB	674	AGATGCTGAAGGTGGGGCCACCCTCACAGGGTTTGGCGAACTGCTCTCGACCAACAACCT	733
QY	661	CTGTCCGCTCAGCGCGCCCAACCAAGGCAATGCACTACTATCTAAGCAGCCAGGACTTCG	720
DB	734	CTGTCCGCTCAGCGCGCCCAACCAAGGCAATGCACTACTATCTAAGCAGCCAGGACTTCG	793
QY	721	ACAGCTCTCTCAGAGGCAGGAGTCAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTTT	780
DB	794	ACAGCTCTCTCAGAGGCAGGAGTCAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTTT	853
QY	781	TTGGCTTTGACATGTGGCAACCTCTCTTCATCTCTCGGAAGGAGTATCTGACGCGGC	840
DB	854	TTGGCTTTGACATGTGGCAACCTCTCTTCATCTCTCGGAAGGAGTATCTGACGCGGC	913
QY	841	AGGAGCGCTCGGCTCAAGCAGATGACAGGAGGAGTCCAGAGCATCAGGCCCAAGCTGC	900
DB	914	AGGAGCGCTCGGCTCAAGCAGATGACAGGAGGAGTCCAGAGCATCAGGCCCAAGCTGC	973
QY	901	TGAGCCGAGCCAGCCTGAGGACAGGAGAGTCTGAAGAGCGCCTGTAGTGTCTCGA	960
DB	974	TGAGCCGAGCCAGCCTGAGGACAGGAGAGTCTGAAGAGCGCCTGTAGTGTCTCGA	1033
QY	961	GCAGCTTCAAGTCTCGGCTCTTTCTGGAGTCGGGCAAGTTGTTCTGTCGACCGAGTCT	1020
DB	1034	GCAGCTTCAAGTCTCGGCTCTTTCTGGAGTCGGGCAAGTTGTTCTGTCGACCGAGTCT	1093
QY	1021	ACC CGGCTTGCCAGAGCCCAAGAAGTGCCTATCTGCAGACAGGCGCATCACCCGGGTGA	1080
DB	1094	ACC CGGCTTGCCAGAGCCCAAGAAGTGCCTATCTGCAGACAGGCGCATCACCCGGGTGA	1153
QY	1081	TACCCCTGTACAA CAGCTAATAGTTTGGAGCCGCA CAGTTGACTGTGAAGACACCCCTG	1140
DB	1154	TACCCCTGTACAA CAGCTAATAGTTTGGAGCCGCA CAGTTGACTGTGAAGACACCCCTG	1213
QY	1141	CCCCCTTTTCAGGGATTTTATCTCGAGGCTTTTGGAGGACGAGTGTGGGGTAGCTGT	1200
DB	1214	CCCCCTTTTCAGGGATTTTATCTCGAGGCTTTTGGAGGACGAGTGTGGGGTAGCTGT	1273
QY	1201	CACCTTCAGGTATGATTGAGGGAGGAATTTGGGTAGAACTCTCCAGACCCCATGCTCCAA	1260
DB	1274	CACCTTCAGGTATGATTGAGGGAGGAATTTGGGTAGAACTCTCCAGACCCCATGCTCCAA	1333
QY	1261	TGGCAGGATGCTGCTTTTCCACCTGAGAGGGGACCTGTCTCCAGAGCCCATCAGA	1320
DB	1334	TGGCAGGATGCTGCTTTTCCACCTGAGAGGGGACCTGTCTCCAGAGCCCATCAGA	1393
QY	1321	GCCTCACCTGGGAGGATGCGGTGGCGTCTCTCCAGAGCCCATCAGTGCAGGTGTG	1380
DB	1394	GCCTCACCTGGGAGGATGCGGTGGCGTCTCTCCAGAGCCCATCAGTGCAGGTGTG	1453
QY	1381	ACTGAAATGCCTCATCACTTAAGCA CCAAGCCAGTGTATCAGCAGCTCTTCTGTTCTGT	1440
DB	1454	ACTGAAATGCCTCATCACTTAAGCA CCAAGCCAGTGTATCAGCAGCTCTTCTGTTCTGT	1513
QY	1441	TGCTCTCTGTTTCTTCTGTTGAACTCGTGTCTGTGACTTGTGGAGGACTCAGAG	1500
DB	1514	TGCTCTCTGTTTCTTCTGTTGAACTCGTGTCTGTGACTTGTGGAGGACTCAGAG	1573
QY	1501	GGGAGGAAAGCTGGGCCCCGAGTACAA CCGATGCTTGGGTGCTCTCCGAGAGACT	1560
DB	1574	GGGAGGAAAGCTGGGCCCCGAGTACAA CCGATGCTTGGGTGCTCTCCGAGAGACT	1633
QY	1561	CTGCCGAGCTTTCTCTTTTCTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAAATGT	1620
DB	1634	CTGCCGAGCTTTCTCTTTTCTTCTCATGCCCCGGGAAACAGTCTTCTTCAGAAATGT	1693

QY	1621	CAGCGTGGCAGGCTCAACTTGTGTTCTTTCCCTCCACTGCTTGCCTTCTTAACGCGTG	1680
Db	1694	CAGCGTGGCAGGCTCAACTTGTGTTCTTTCCCTCCACTGCTTGCCTTCTTAACGCGTG	1753
QY	1681	CACGTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACACATCCGCTTCTGCCAGATGGT	1740
Db	1754	CACGTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACATCCGCTTCTGCCAGATGGT	1813
QY	1741	CGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTTGGTCAGGCAGGCC	1800
Db	1814	TGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGGCAGTTGGTCAGGCAGGCC	1873
QY	1801	TCCTGGTTTTCCGCACTGCGCCCTGATTTGAACTCCTCGCCACTGCGGAGAGCTCGGGTGGT	1860
Db	1874	TCCTGGTTTTCCGCACTGCGCCCTGATTTGAACTCCTCGCCACTGCGGAGAGCTCGGGTGGT	1933
QY	1861	CCCTGGTTTTCCCTCTCGGAGATGAGGCGCAGAGGCTCGCGCTCTCTGAAGGACGCGATG	1920
Db	1934	CCCTGGTTTTCCCTCTCGGAGATGAGGCGCAGAGGCTCGCGCTCTCTGAAGGACGCGATG	1993
QY	1921	TGGATGCCACTGGCCTAGTGTCTCGGCTCACAGCTTCTTGAAGGCTGTCAAGGAA	1980
Db	1994	TGGATGCCACTGGCCTAGTGTCTCGGCTCACAGCTTCTTGAAGGCTGTCAAGGAA	2053
QY	1981	AAGCAGCGGGCTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGTCG	2040
Db	2054	AAGCAGCGGGCTGGCACCCCTGAGCATATGCCCTCTTGGGCTCCCTCATCCAGCCCGTCG	2113
QY	2041	CAGCTTTGACATCTTGTGTGTAATGTCCTCTCTCTGTGTACCCCTCCAGTATT	2100
Db	2114	CAGCTTTGACATCTTGTGTGTAATGTCCTCTCTCTGTGTACCCCTCCAGTATT	2173
QY	2101	ACCAATTTGCCCTCACCTGCCCTTGGTGAGCCTTTAGTGCAGACAGATGGGGCTGTTT	2160
Db	2174	ACCAATTTGCCCTCACCTGCCCTTGGTGAGCCTTTAGTGCAGACAGATGGGGCTGTTT	2233
QY	2161	TCCCCCACTCTGAGTAGTTGGAGGTACATACACAGCTCTTTTATTGGCCCTTTTCT	2220
Db	2234	TCCCCCACTCTGAGTAGTTGGAGGTACATACACAGCTCTTTTATTGGCCCTTTTCT	2293
QY	2221	GCCTCTCAAGTTTCATCTCTCGTCCCTCTTGTGTGAGGAGGAGGGGTGCCCTCAGGG	2280
Db	2294	GCCTCTCAAGTTTCATCTCTCGTCCCTCTTGTGTGAGGAGGAGGGGTGCCCTCAGGG	2353
QY	2281	GCCGACACTAGTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACAATGTTGCAAC	2340
Db	2354	GCCGACACTAGTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACAATGTTGCAAC	2413
RESULT 5			
ABQ91949			
ID	ABQ91949 standard; cdna; 2401 BP.		
AC	ABQ91949;		
XX			
DT	30-SEP-2002 (first entry)		
DE	Human NF-kB activating gene SEQ ID NO 76.		
XX			
KW	Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;		
KW	immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;		
KW	neuroprotective; anti-HIV; autoimmune disease; cancer; infection;		
KW	bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;		
OS	Homo sapiens.		
XX			
XX			
PN	W0200253737-A1.		
XX			
PD	11-JUL-2002.		
XX			
PF	25-DEC-2001; 2001WO-JP011389.		
XX			

PR 28-DEC-2000; 2000JP-00402288.
 PR 26-MAR-2001; 2001JP-00089912.
 PR 24-AUG-2001; 2001JP-00254018.
 XX
 PA (ASAH) ASAH KASEI KOGYO KK.
 XX
 PI Matsuda A, Honda G, Muramatsu S, Nagano Y;
 XX
 DR WPI; 2002-583617/62.
 DR P-PSDB; ABP61461.
 XX
 XX NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.
 XX
 PS Claim 4; Page 352-357; 841pp; Japanese.
 XX
 CC The invention relates to a purified protein (I), comprising one of 90
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 CC the sequences but with some amino acids deleted, substituted or added and
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and
 CC encoding gene (ABO91912-ABO92001) are useful in diagnosis and screening
 CC inhibitors or promoters to control excessive activation or inhibition and
 CC for treating e.g. inflammations, autoimmune diseases, cancers, or ischaemic
 CC infections, bone diseases, AIDS, neurodegenerative diseases or disorders
 XX
 SQ Sequence 2401 BP; 485 A; 664 C; 697 G; 555 T; 0 U; 0 Other;
 Query Match 99.2%; Score 2336.8; DB 6; Length 2401;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 ATCTCTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGTCTCATGGAGAGCGAGGGGCGC 60
 62 ATCTCTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGTCTCATGGAGAGCGAGGGGCGC 121
 61 CCTCGCTGTGCCAGTTCATCTCTCTGGGACACCTCTGTGGTTCACCGCGCCCTGTACT 120
 122 CCTCGCTGTGCCAGTTCATCTCTCTGGGACACCTCTGTGGTTCACCGCGCCCTGTACT 181
 121 CCGGTACCGGCAGAGCGCGGCTCTCCAGAGCTCAAGGAGCTTAAAGTTCATT 180
 182 CCGGTACCGGCAGAGCGCGGCTCTCCAGAGCTCAAGGAGCTTAAAGTTCATT 241
 181 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGTCTCAGGAAATCGCTGTATGCTG 240
 242 TGGGTGAAGATTTAAAGAGTATCTTTTCAAGAGTCTCAGGAAATCGCTGTATGCTG 301
 241 TTATAGAGAGGAGCTGTGGGCTGTGTAAAGAAACGCTTAAAGAGCTTGTGGAAACT 300
 302 TTATAGAGAGGAGCTGTGGGCTGTGTAAAGAAACGCTTAAAGAGCTTGTGGAAACT 361
 301 GCAAGGGGTAAATTCAGCGGCTGACATTTCAAGAGCAAGAGTGTGGAAATCGAACCA 360
 362 GCAAGGGGTAAATTCAGCGGCTGACATTTCAAGAGCAAGAGTGTGGAAATCGAACCA 421
 361 CCCACCTTTTGAATGATCTCAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG 420
 422 CCCACCTTTTGAATGATCTCAAGATCAATTCATCAGAGGACCAACACAGTGCCTTTG 481
 421 ACCTGGTCCCAACAGAGTGGGTGGATGTGGCTGTGGAGTGTGAAGCCCTTGGACT 480
 482 ACCTGGTCCCAACAGAGTGGGTGGATGTGGCTGTGGAGTGTGAAGCCCTTGGACT 541
 481 CAGTGGATCTGGGTCTAGAGATCTGTATGAGAGTTCACCCCTCGATTCACTCTTCA 540
 542 CAGTGGATCTGGGTCTAGAGATCTGTATGAGAGTTCACCCCTCGATTCACTCTTCA 601
 541 CCGATGTATCGGCGCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACCGAGG 600
 602 CCGATGTATCGGCGCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACCGAGG 661

QY 601 AGATGCTGAGGTGGGGGCCACCTCAAGGGGTGGCGAAGTCTCTGCAACAACT 660
 DB 662 AGATGCTGAGGTGGGGGCCACCTCAAGGGGTGGCGAAGTCTCTGCAACAACT 721
 QY 661 CTGTCCGCTGTGAGCGCGCCCAACAGGCATGAGGTACTATCTAAGCAGCAGGACTTCG 720
 DB 722 CTGTCCGCTGTGAGCGCGCCCAACAGGCATGAGGTACTATCTAAGCAGCAGGACTTCG 781
 QY 721 ACAGCCTGTGAGCGCGCCCAACAGGCATGAGGTACTATCTAAGCAGCAGGACTTCG 780
 DB 782 ACAGCCTGTGAGCGCGCCCAACAGGCATGAGGTACTATCTAAGCAGCAGGACTTCG 841
 QY 781 TTGGCTTTGCGCATGTGCGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 DB 842 TTGGCTTTGCGCATGTGCGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 901
 QY 841 AGGAGCGCTTGGCGCTCAAGCAGATGAGGAGGAGTTCCAGGAGCATGAGGCCAGCTGC 900
 DB 902 AGGAGCGCTTGGCGCTCAAGCAGATGAGGAGGAGTTCCAGGAGCATGAGGCCAGCTGC 961
 QY 901 TGAGCCGAGCCAAAGCCTGAGGACAGGAGAGTCTGAAGAGGCGCTGTGTGTCTGA 960
 DB 962 TGAGCCGAGCCAAAGCCTGAGGACAGGAGAGTCTGAAGAGGCGCTGTGTGTCTGA 1021
 QY 961 GCAGCTTCAAGTCTCTGCT 1020
 DB 1022 GCAGCTTCAAGTCTCTGCT 1081
 QY 1021 ACCCGCGCTTGGCGAGCCCAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGTGA 1080
 DB 1082 ACCCGCGCTTGGCGAGCCCAAGAGTGCCTTATCTGCAGACAGGCGATCACCCGGTGA 1141
 QY 1081 TACCCCTGTGACAAAGCTATAGTTTGAAGCCGACAGCTTGAACCTTGAAGACACCCCTG 1140
 DB 1142 TACCCCTGTGACAAAGCTATAGTTTGAAGCCGACAGCTTGAACCTTGAAGACACCCCTG 1201
 QY 1141 CCCCCTTTTCAAGGATTTTATCTCGAGGCTTTTGGAGGAGCAGTGTGTGGGGTGTAGTGT 1200
 DB 1202 CCCCCTTTTCAAGGATTTTATCTCGAGGCTTTTGGAGGAGCAGTGTGTGGGGTGTAGTGT 1261
 QY 1201 CACCTCCAGGTATGATTGAGGAGGAAATGGGTAGAACTCTCCAGACCCATGCTCCAA 1260
 DB 1262 CACCTCCAGGTATGATTGAGGAGGAAATGGGTAGAACTCTCCAGACCCATGCTCCAA 1321
 QY 1261 TGGCAGGATGTGCTTTCACCTGTGAGAGGAGCCCTGTCCATGTGAGGCTCATCAGA 1320
 DB 1322 TGGCAGGATGTGCTTTCACCTGTGAGAGGAGCCCTGTCCATGTGAGGCTCATCAGA 1381
 QY 1321 GCCTCACCTGGGAGGATGCGTGGCGTCTCTCCAGAGGAGCCAGATCAGTGCAGTGTG 1380
 DB 1382 GCCTCACCTGGGAGGATGCGTGGCGTCTCTCCAGAGGAGCCAGATCAGTGCAGTGTG 1441
 QY 1381 ACTGAAATGCTCATCATCTTAAGCAACAAAGCAGTGTGAGGAGTCTTCTGTGCTGTG 1440
 DB 1442 ACTGAAATGCTCATCATCTTAAGCAACAAAGCAGTGTGAGGAGTCTTCTGTGCTGTG 1501
 QY 1441 TGTCTTCTGTTTTTCTGTTGTAATCGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1500
 DB 1502 TGTCTTCTGTTTTTCTGTTGTAATCGTTGCTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1561
 QY 1501 GGGAGGAAAGCTGGGGCCCGAGTACAAAGGATGCTTTGGGTGTGCTTCCGAGAGACT 1560
 DB 1562 GGGAGGAAAGCTGGGGCCCGAGTACAAAGGATGCTTTGGGTGTGCTTCCGAGAGACT 1621
 QY 1561 CTGCGCAGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1620
 DB 1622 CTGCGCAGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1681
 QY 1621 CAGGTGGGAGGTCAGTGTGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1680
 DB 1682 CAGGTGGGAGGTCAGTGTGTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1741

QY 1681 CACGTGTGTGTAGAGACAAAAGAGTGAAGTCAGACATCGCTTCTGCCAGATGT 1740
 Db |||||
 QY 1742 CACGTGTGTGTAGAGACAAAAGAGTGAAGTCAGACATCGCTTCTGCCAGATGT 1801
 Db |||||
 QY 1741 CGGGCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTGTGTCAGGCGCC 1800
 Db |||||
 QY 1802 CGGGCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTGTGTCAGGCGCC 1861
 Db |||||
 QY 1801 TCTCGTTTGGCCACTGGCCCTGATTGAACTCCCTGCCACTGGGAGAGCTGGGTGT 1860
 Db |||||
 QY 1862 TCTCGTTTGGCCACTGGCCCTGATTGAACTCCCTGCCACTGGGAGAGCTGGGTGT 1921
 Db |||||
 QY 1861 CCCTGGTTTCCCTCCTCGAGAAATGAGGCGAGAGGCTCGCTCTGAAAGACAGTGT 1920
 Db |||||
 QY 1922 CCCTGGTTTCCCTCCTCGAGAAATGAGGCGAGAGGCTCGCTCTGAAAGACAGTGT 1981
 Db |||||
 QY 1921 TGGATGCCACTGGCTAGTGTCTGGCTCAGAGTCTCTGCAAGGCTGTCAAGGAA 1980
 Db |||||
 QY 1982 TGGATGCCACTGGCTAGTGTCTGGCTCAGAGTCTCTGCAAGGCTGTCAAGGAA 2041
 Db |||||
 QY 1981 AAGCAGCGGCTGGCACCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCCTG 2040
 Db |||||
 QY 2042 AAGCAGCGGCTGGCACCCTGAGCATATGCCCTCTTGGGGCTCCCTCATCAGCCCTG 2101
 Db |||||
 QY 2041 CAGCTTGAACATCTGGTGTACTCATGTCGCTTCTCTTGTGTTACCCCTCCAGTAT 2100
 Db |||||
 QY 2102 CAGCTTGAACATCTGGTGTACTCATGTCGCTTCTCTTGTGTTACCCCTCCAGTAT 2161
 Db |||||
 QY 2101 ACCATTTGCCCTCAGCTGCCCTTGGTGTGAGCTTTTAGTGAACAGATGGGCTGTT 2160
 Db |||||
 QY 2162 ACCATTTGCCCTCAGCTGCCCTTGGTGTGAGCTTTTAGTGAACAGATGGGCTGTT 2221
 Db |||||
 QY 2161 TCCGCCACCTCTGAGTGTGAGGTCAATACAGCTCTTTTATTGCCCCCTTTCT 2220
 Db |||||
 QY 2222 TCCGCCACCTCTGAGTGTGAGGTCAATACAGCTCTTTTATTGCCCCCTTTCT 2281
 Db |||||
 QY 2221 GCCTCTGAATGTTCACTCTGCTCTCTTGTGAGGAGGAGGAGGCTGCTCAGGG 2280
 Db |||||
 QY 2282 GCCTCTGAATGTTCACTCTGCTCTCTTGTGAGGAGGAGGAGGCTGCTCAGGG 2341
 Db |||||
 QY 2281 GCCGACACTAGTATGAGTGTCCAGTGTGAAACAGAGAAATTAACATGTTGCAACC 2340
 Db |||||
 QY 2342 GCCGACACTAGTATGAGTGTCCAGTGTGAAACAGAGAAATTAACATGTTGCAACC 2401

RESULT 6
 ID ABQ91948
 AC ABQ91948 standard; cDNA; 2401 BP.
 XX ABQ91948;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human NF-kB activating gene SEQ ID NO 74.
 XX
 KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;
 SS.
 XX
 OS Homo sapiens.
 XX
 PN WO200253737-A1.
 XX
 PD 11-JUL-2002.
 XX
 XX 25-DEC-2001; 2001WO-JP011389.
 PF
 XX 28-DEC-2000; 2000JP-00402288.
 PR
 XX 26-MAR-2001; 2001JP-00089312.
 PR
 XX 24-AUG-2001; 2001JP-00254018.
 PR
 XX

(ASAH) ASahi KASEI KOGYO KK.

Matsuda A, Honda G, Muramatsu S, Nagano Y;

WPI: 2002-583617/62.

P-PSDB; ABP61460.

NF-approximatelykB activating gene and expressed protein, applicable in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition for treating e.g. inflammations, autoimmune diseases and cancer.

Claim 4; Page 345-349; 841pp; Japanese.

The invention relates to a purified protein (I), comprising one of 90 fully defined sequences (ABP61424-ABP61513) or a protein based on any of the sequences but with some amino acids deleted, substituted or added and with a NF-kB (nuclear factor kappa B) activating effect. The protein and encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition and for treating e.g. inflammations, autoimmune diseases, cancers, infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic disorders

Sequence 2401 BP; 485 A; 665 C; 697 G; 554 T; 0 U; 0 Other;

Query Match 99.1%; Score 2335.2; DB 6; Length 2401;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2337; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATCCTTGGCGCCACAGTCGGCCACCGGGGTGCGCCGCTCATGGAGCGAGGGGGC 60
 Db 62 ATCCTTGGCGCCACAGTCGGCCACCGGGGTGCGCCGCTCATGGAGCGAGGGGGC 121
 QY 61 CCTCGCTGTCGCCATTCCTCTCTGGGACCACTCTGTGGTCAACCGCCCTGTACT 120
 Db 122 CCTCGCTGTCGCCATTCCTCTCTGGGACCACTCTGTGGTCAACCGCCCTGTACT 181
 QY 121 CCTGTACCGCGCAGAGGCGCGGTCTCCCAAGAGTCAAGGAGCTTAAAGATTCATT 180
 Db 182 CCTGTACCGCGCAGAGGCGCGGTCTCCCAAGAGTCAAGGAGCTTAAAGATTCATT 241
 QY 181 TGGGTGAAGATTTAAAGAGTATTTCTTTCAAGCTCCAGGAAATGCTCTATCTG 240
 Db 242 TGGGTGAAGATTTAAAGAGTATTTCTTTCAAGCTCCAGGAAATGCTCTATCTG 301
 QY 241 TTATAGAGGAGCTGTGCGGTCTGTTAAAGAAACGCTTACAGCCAGTTTGTGAAACT 300
 Db 302 TTATAGAGGAGCTGTGCGGTCTGTTAAAGAAACGCTTACAGCCAGTTTGTGAAACT 361
 QY 301 GCAAGGGGTAAATTCAAGCGGCTGACACTTCAGGAGCACAAGATGCTGGAATCGAACCA 360
 Db 362 GCAAGGGGTAAATTCAAGCGGCTGACACTTCAGGAGCACAAGATGCTGGAATCGAACCA 421
 QY 361 CCACCTTTGGAATGATGCTCAAGATCATTCATCAGAGGACCAACAGTGCCTTTG 420
 Db 422 CCCACCTTTGGAATGATGCTCAAGATCATTCATCAGAGGACCAACAGTGCCTTTG 481
 QY 421 ACCTGTGCCCCCAGGAGTGGGTGATGTGGTGTGCGAGTGTGAAGCCCTGACT 480
 Db 482 ACCTGTGCCCCCAGGAGTGGGTGATGTGGTGTGCGAGTGTGAAGCCCTGACT 541
 QY 481 CAGTGTATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCAGTCTTCA 540
 Db 542 CAGTGTATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGATTTCAGTCTTCA 601
 QY 541 CCGATGTATCTGGCCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACGAGG 600
 Db 602 CCGATGTATCTGGCCACTACATCAGCGGTGAGCGGCCCAAGGCAATCCAGAGACGAGG 661
 QY 601 AGATCTGAAGTGGGGGCCACCTCAGAGGGTTGGCGAACTGTCTCTGGCAACAACACT 660
 Db 662 AGATCTGAAGTGGGGGCCACCTCAGAGGGTTGGCGAACTGTCTCTGGCAACAACACT 721

661	CTGTCCGCTGCAGCGGCCAAACAAGGCAATGCAGTACTATCTAAGCAGCAGGACTTCG	720
722	CTGTCCGCTGCAGCGGCCAAACAAGGCAATGCAGTACTATCTAAGCAGCAGGACTTCG	781
721	ACAGCTGCTGCAGAGCGAGGAGTCAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTT	780
782	ACAGCTGCTGCAGAGCGAGGAGTCAGCGTCAGGCTCTGGAAGGTGCTGGCGCTGGTT	841
781	TTGGCTTTGCCATGTGCCACCTCTTTCTTCTTCTTCTCCGGAAGCAGTATCTCAGCGGC	840
842	TTGGCTTTGCCATGTGCCACCTCTTTCTTCTTCTTCTCCGGAAGCAGTATCTCAGCGGC	901
841	AGGAGCGCTTGCGCCCTCAAGCAGATGCAGAGAGTTCCAGGAGCATGAGGCCAGTGC	900
902	AGGAGCGCTTGCGCCCTCAAGCAGATGCAGAGAGTTCCAGGAGCATGAGGCCAGTGC	961
901	TGAGCCGAGCGAAGCTTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA	960
962	TGAGCCGAGCGAAGCTTGAGGACAGGAGAGTCTGAAGAGCGCTGTGTAGTGTCTGA	1021
961	GCAGCTTCAAGTCTCTGGTCTTTCTGAGTGTGGCACGTTTGTTCCTGCAACGAGTGCT	1020
1022	GCAGCTTCAAGTCTCTGGTCTTTCTGAGTGTGGCACGTTTGTTCCTGCAACGAGTGCT	1081
1021	ACCGCGCTTTGCCAGAGCCCAAGAAGTGCCCTATCTGCAGACAGCGCATACCCGGGTGA	1080
1082	ACCGCGCTTTGCCAGAGCCCAAGAAGTGCCCTATCTGCAGACAGCGCATACCCGGGTGA	1141
1081	TACCCCTGTACAACAGCTAATAGTTTGGAGCCGCACAGCTTGTACCTGGGAAGCACCCCTG	1140
1142	TACCCCGCTACAACAGCTAATAGTTTGGAGCCGCACAGCTTGTACCTGGGAAGCACCCCTG	1201
1141	CCCCCTTTTCAGGGAATTTTATCTCGAGGCCCTTTGGAGGACGAGTGTGGGGGTAGCTGT	1200
1202	CCCCCTTTTCAGGGAATTTTATCTCGAGGCCCTTTGGAGGACGAGTGTGGGGGTAGCTGT	1261
1201	CACCTCCAGGTATGATTGAGGGAGGAATGGGTAGAAACTCTCAGACCCATGCTCCAA	1260
1262	CACCTCCAGGTATGATTGAGGGAGGAATCGGGTAGAAACTCTCCAGACCCATGCTCCAA	1321
1261	TGGCAGATGCTGCTTTTCCACCTGAGAGGGACCTGTCCATGTGCAGCTCATCAGA	1320
1322	TGGCAGATGCTGCTTTTCCACCTGAGAGGGACCCCTGTCCATGTGCAGCTCATCAGA	1381
1321	GCCTCACCTCGGAGGATCGGTGCGTCTCTCTCCAGAGCCAGATCAGTGCAGTGTG	1380
1382	GCCTCACCTCGGAGGATCGCTGCGTCTCTCTCCAGAGCCAGATCAGTGCAGTGTG	1441
1381	ACTGAAATGCTCATCATCTTAAGCACCAAGCCAGTGATCAGCAGCTCTTCTGTCTGTG	1440
1442	ACTGAAATGCTCATCATCTTAAGCACCAAGCCAGTGATCAGCAGCTCTTCTGTCTGTG	1501
1441	TGCTCTCTGTTTTTTTCTGGTGAATCGTTGCTGTGGAATTGGTGGAGGACTCAGAG	1500
1502	TGCTCTCTGTTTTTTTCTGGTGAATCGTTGCTGTGGAATTGGTGGAGGACTCAGAG	1561
1501	GGGAGGAAGGCTGGGCCCGCAGTACAACGGATGCTTGGGTGCTGCTCCGAAGAGACT	1560
1562	GGGAGGAAGGCTGGGCCCGCAGTACAACGGATGCTTGGGTGCTGCTCCGAAGAGACT	1621
1561	CTGCGCAGCTTTTCTCTTTTTTCTCTATGCCCCGGGAAACAGTCTTTTCTCAGAAATGTT	1620
1622	CTGCGCAGCTTTTCTCTTTTTTCTCTATGCCCCGGGAAACAGTCTTTTCTCAGAAATGTT	1681
1621	CAGGCTGGCAGGTCAACTGTGTGTTCTTTTCCCTCACCTGCTGGCTCTTAAACGCTG	1680
1682	CAGGCTGGCAGGTCAACTGTGTGTTCTTTTCCCTCACCTGCTGGCTCTTAAACGCTG	1741
1681	CACGTGTGTGTAGAGACAAAAGAAAGTGAAGTCAGCACATCCGCTTCTGCCAGATGGT	1740
1742	CACGTGTGTGTAGAGACAAAAGAAAGTGAAGTCAGCACATCCGCTTCTGCCAGATGGT	1801

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 8; SEQ ID NO 14872; 2537pp + Sequence Listing; English.
vz

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB932446 to AAB958993 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

SQ Sequence 2442 BP; 498 A; 673 C; 706 G; 565 T; 0 U; 0 Other;

Query Match 99.0%; Score 2332; DB 4; Length 2442;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 2335; Conservative 0; Mismatches 5; Index 0

[illegible]

1	ATCTTGGGCCACAGTCGGCCACCGGGGCTCGCGCCGT	CATCGAGAGCGAGGGCGC	60
103	ATCTTGGGCCACAGTCGGCCACCGGGGCTCGCGCCGT	CATCGAGAGCGAGGGCGC	162
61	CTCTCGTGTGCCAGTTTCATCTCTTGGGCAACCACT	CTGTGGTCAACCGCGCCCTGTACT	120
163	CTCTCGTGTGCCAGTTTCATCTCTTGGGCAACCACT	CTGTGGTCAACCGCGCCCTGTACT	222
121	CGGTGTACCGGCAGAAAGGCCGGGTCTCCCAAGAGCT	CAAGGGAGCTAAAAAGTTCATT	180
223	CGGTGTACCGGCAGAAAGGCCGGGTCTCCCAAGAGCT	CAAGGGAGCTAAAAAGTTCATT	282
181	TGGGTGAAGATTAAAGAGTATTTCTTT	CAGAAGCTCCAGGAAATCGTGCTTATGCTG	240
283	TGGGTGAAGATTAAAGAGTATTTCTTT	CAGAAGCTCCAGGAAATCGTGCTTATGCTG	342
241	TTATAGAAGGAGCTGTGGGTCTGTTTAAAGAAACG	TTAACGCCAGTTTGTGAAAAACT	300
343	TTATAGAAGGAGCTGTGGGTCTGTTTAAAGAAACG	TTAACGCCAGTTTGTGAAAAACT	402
301	GCAAGGGGTAAATTCAGCGGTGCACACTT	CAGAGCACAGATGGTGTGGAATCGAACCA	360
403	GCAAGGGGTAAATTCAGCGGTGCACACTT	CAGAGCACAGATGGTGTGGAATCGAACCA	462
361	CCCACTTTGGGAATGATTGCTCAAAGATCATTCAT	CAGAGGACCAACACAGTGCCTTTG	420
463	CCCACTTTGGGAATGATTGCTCAAAGATCATTCAT	CAGAGGACCAACACAGTGCCTTTG	522
421	ACCTGGTGCCCAACGAGGATGGCGTGGAATGTGCT	GTGGAGTGCTGAAGCCCTTGACT	480
523	ACCTGGTGCCCAACGAGGATGGCGTGGAATGTGCT	GTGGAGTGCTGAAGCCCTTGACT	582
481	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAGTT	TCCACCCCTGATTCAGTCTTCA	540
593	CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAGTT	TCCACCCCTGATTCAGTCTTCA	642

Db 565 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCCACCCCTCGAATTCAGTCCTTCA 624
QY 541 CCATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGATCCAAAGAGACCGAGG 600
Db 625 CCATGTCATCGGCCACTACATCAGCGGTGAGCGGCCCAAGGATCCAAAGAGACCGAGG 684
QY 601 AGATGCTGAAGAGTGGGGGCCACCCCTCACAGGGGTGGCGAACTGGTCTCGACAAACAAT 660
Db 685 AGATGCTGAAGAGTGGGGGCCACCCCTCACAGGGGTGGCGAACTGGTCTCGACAAACAAT 744
QY 661 CTGTCCGCTGAGCGGCCCAAAACAGGCAATGCACTACTATCTAAGCAGCAGGACTTCG 720
Db 745 CTGTCCGCTGAGCGGCCCAAAACAGGCAATGCACTACTATCTAAGCAGCAGGACTTCG 804
QY 721 ACAGCCTGCTGAGAGCAGAGTCTCAGCGTCTGAGAGTCTGGAAGTGGTCTGGCGCTGGTTT 780
Db 805 ACAGCCTGCTGAGAGCAGAGTCTCAGCGTCTGAGAGTCTGGAAGTGGTCTGGCGCTGGTTT 864
QY 781 TTGGCTTTGCCACATGTGGCCACCTCTCTTCTTCAATCTCCGGAAGCAGTATCTCAGCGGC 840
Db 865 TTGGCTTTGCCACATGTGGCCACCTCTCTTCTTCAATCTCCGGAAGCAGTATCTCAGCGGC 924
QY 841 AGAGCGCCTGCGCCT-CAAGCAGTGCAGAGGATCTCAGAGCATGAGGCCAGCTG 899
Db 925 AGAGCGCCTGCGCCTGCAAGCAGTGCAGAGGATCTCAGAGCATGAGGCCAGCTG 984
QY 900 CTGAGCGCAGCCAAAGCTCAGGACAGGAGTCTGAGAGGATCTGGAAGCGCCTGTGTGTGTCTG 959
Db 985 CTGAGCGGAGCCAAAGCTCAGGACAGGAGTCTGGAAGCGCCTGTGTGTGTCTG 1044
QY 960 AGCAGCTTCAAGTCTCGCTCTTTCTGGAGTGTGGGACGTTTGTCTCGACCGAGTGC 1019
Db 1045 AGCAGCTTCAAGTCTCGCTCTTTCTGGAGTGTGGGACGTTTGTCTCGACCGAGTGC 1104
QY 1020 TACCGCGCTTGCAGAGCCAAAGAGTGCCTTATCTGAGCAGCGCATACCCGGGTG 1079
Db 1105 TACCGCGCTTGCAGAGCCAAAGAGTGCCTTATCTGAGCAGCGCATACCCGGGTG 1164
QY 1080 ATACCCCTCTCAACAGCTAATAGTTTGAAGCCGACAGCTTGACCTGGAGCACCCT 1139
Db 1165 ATACCCCTCTCAACAGCTAATAGTTTGAAGCCGACAGCTTGACCTGGAGCACCCT 1224
QY 1140 GCCCCCTTTTCAAGGATTTTATCTCGAGCGCTTTTGGAGGACAGTGTGGGGTAGCTG 1199
Db 1225 GCCCCCTTTTCAAGGATTTTATCTCGAGCGCTTTTGGAGGACAGTGTGGGGTAGCTG 1284
QY 1200 TCACCTCCAGGTATGATTGAGGAGAAATTGGTAGAAACTCTCCAGACCCATGCTCCA 1259
Db 1285 TCACCTCCAGGTATGATTGAGGAGAAATTGGTAGAAACTCTCCAGACCCATGCTCCA 1344
QY 1260 ATGGCAGGATGCTGCTTTCCACCTGAGAGGGACCTGTCATGTGAGCGCTCATCAG 1319
Db 1345 ATGGCAGGATGCTGCTTTCCACCTGAGAGGGACCTGTCATGTGAGCGCTCATCAG 1404
QY 1320 AGCCTCACCTGGAGGATGCGGTGGCGTCTCTCCAGAGCCAGATCAGTGCAGTGT 1379
Db 1405 AGCCTCACCTGGAGGATGCGGTGGCGTCTCTCCAGAGCCAGATCAGTGTGAGTGT 1464
QY 1380 GACTGAAATGCTCATCATTTAAGACCAAGCCAGTGATCAGAGCTCTTCTGTCTCT 1439
Db 1465 GACTGAAATGCTCATCATTTAAGACCAAGCCAGTGATCAGAGCTCTTCTGTCTCT 1524
QY 1440 GTGTCTCTGTTTTTTTCTGGTGAATCGTTGCTGTGGACTTGGTGGAGCTCAGA 1499
Db 1525 GTGTCTCTGTTTTTTTCTGGTGAATCGTTGCTGTGGACTTGGTGGAGCTCAGA 1584
QY 1500 GGGAGGAAAGCTGGGGCCCGAGTACACAGGATGCTTGGTGTGCTCTCGAAGAGAC 1559
Db 1585 GGGAGGAAAGCTGGGGCCCGAGTACACAGGATGCTTGGTGTGCTCTCGAAGAGAC 1644
QY 1560 TCTGCCGAGCTTTTCTTTTCTCTCATGCCCGGAAACAGTCTTTCTTCAAGATTG 1619
Db 1645 TCTGCCGAGCTTTTCTTTTCTCTCATGCCCGGAAACAGTCTTTCTTCAAGATTG 1704

QY 1620 TCAGGCTGGCAGGTCAACTTGTGTTCTTTCCTTCCCTCACCTGTGCTTCCCTTAACGCCT 1679
Db 1705 TCAGGCTGGCAGGTCAACTTGTGTTCTTTCCTTCCCTCACCTGTGCTTCCCTTAACGCCT 1764
QY 1680 GCAGCTGTGTGTAGAGCAAAAGAAAGTGAAGTCAAGCATCGCTTCTGCCAGATGG 1739
Db 1765 GCAGCTGTGTGTAGAGCAAAAGAAAGTGAAGTCAAGCATCGCTTCTGCCAGATGG 1824
QY 1740 TCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCAAGTGTGTCAAGCAGGC 1799
Db 1825 TCGGGGCCCCGGGCAACAGATTGAAGAGAGATCATGTGAAGGCAAGTGTGTCAAGCAGGC 1884
QY 1800 CTCCTGGTTTGGCCACTGGCCCTGATTTGAATCTCTGCCACTTGGGAGAGCTCGGGGTGG 1859
Db 1885 CTCCTGGTTTGGCCACTGGCCCTGATTTGAATCTCTGCCACTTGGGAGAGCTCGGGGTGG 1944
QY 1860 TCCTCTGTTTTCCTCTCTGAGAAATGAGGCGCAGAGGCTCGGCTCTCTGAAGCAGCAGT 1919
Db 1945 TCCTCTGTTTTCCTCTCTGAGAAATGAGGCGCAGAGGCTCGGCTCTCTGAAGCAGCAGT 2004
QY 1920 GTGGATGCCACTGGCCCTAGTGTCTGGCCTCACAGCTTCTTGCAGAGGCTGTCAAGGA 1979
Db 2005 GTGGATGCCACTGGCCCTAGTGTCTGGCCTCACAGCTTCTTGCAGAGGCTGTCAAGGA 2064
QY 1980 AAAGCAGCGGCTGGCACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTC 2039
Db 2065 AAAGCAGCGGCTGGCACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTC 2124
QY 2040 GCAGCTTTCACATCTGGTGTACTCATGTGCTTCTCTTGTGTACCCCTCCCAAGTAT 2099
Db 2125 GCAGCTTTCACATCTGGTGTACTCATGTGCTTCTCTTGTGTACCCCTCCCAAGTAT 2184
QY 2100 TACCATTTCGCCCTCACCTGGCTTGGTGAAGCTTTTGTGCAAGACAGATGGGCTGT 2159
Db 2185 TACCATTTCGCCCTCACCTGGCTTGGTGAAGCTTTTGTGCAAGACAGATGGGCTGT 2244
QY 2160 TTCGCCACCTCTGAGTGTGAGGTCAATACACAGCTCTTTTATGCCCCCTTTC 2219
Db 2245 TTCGCCACCTCTGAGTGTGAGGTCAATACACAGCTCTTTTATGCCCCCTTTC 2304
QY 2220 TCGCTCTGAATGTTTCT 2279
Db 2305 TCGCTCTGAATGTTTCT 2364
QY 2280 GGCCGACACTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAAC 2339
Db 2365 GGCCGACACTAGTATGATGAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAAC 2424
QY 2340 CAAAAA 2346
Db 2425 CAAAAA 2431

RESULT 9

AAS25835

ID AAS25835 standard; cDNA; 2446 BP.

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AC AAS25835;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human cDNA encoding a novel secreted protein, Seq ID 14.

XX

Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;
cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
antibacterial; virucide; fungicide; opthalmological; vulnery;
secreted protein; rheumatoid arthritis; hyperproliferative disorder;
cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
cerebral ischaemia; angiogenesis; nervous system disorder;
Alzheimer's disease; infection; ocular disorder; corneal infection;
wound healing; epithelial cell proliferation; skin ageing; food additive;
preservative; antiproliferative.

XX	Homo sapiens.	
OS	WO200155322-A2.	
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PN		
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PD	02-AUG-2001.	
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PF	17-JAN-2001; 2001WO-US001341.	
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PR	31-JAN-2000; 2000US-0179065P.	
PR	04-FEB-2000; 2000US-0180628P.	
PR	24-FEB-2000; 2000US-0184664P.	
PR	02-MAR-2000; 2000US-0186350P.	
PR	16-MAR-2000; 2000US-0189874P.	
PR	17-MAR-2000; 2000US-0190076P.	
PR	18-APR-2000; 2000US-0198123P.	
PR	19-MAY-2000; 2000US-0205515P.	
PR	07-JUN-2000; 2000US-0209467P.	
PR	28-JUN-2000; 2000US-0214886P.	
PR	30-JUN-2000; 2000US-0215135P.	
PR	07-JUL-2000; 2000US-0216647P.	
PR	07-JUL-2000; 2000US-0216880P.	
PR	11-JUL-2000; 2000US-0217487P.	
PR	11-JUL-2000; 2000US-0217496P.	
PR	14-JUL-2000; 2000US-0218290P.	
PR	26-JUL-2000; 2000US-0220963P.	
PR	26-JUL-2000; 2000US-0220964P.	
PR	14-AUG-2000; 2000US-0224518P.	
PR	14-AUG-2000; 2000US-0224519P.	
PR	14-AUG-2000; 2000US-0225213P.	
PR	14-AUG-2000; 2000US-0225214P.	
PR	14-AUG-2000; 2000US-0225266P.	
PR	14-AUG-2000; 2000US-0225267P.	
PR	14-AUG-2000; 2000US-0225268P.	
PR	14-AUG-2000; 2000US-0225270P.	
PR	14-AUG-2000; 2000US-0225447P.	
PR	14-AUG-2000; 2000US-0225575P.	
PR	14-AUG-2000; 2000US-0225758P.	
PR	14-AUG-2000; 2000US-0225759P.	
PR	18-AUG-2000; 2000US-0226279P.	
PR	22-AUG-2000; 2000US-0226681P.	
PR	22-AUG-2000; 2000US-0226868P.	
PR	23-AUG-2000; 2000US-0227182P.	
PR	23-AUG-2000; 2000US-0227009P.	
PR	30-AUG-2000; 2000US-0228924P.	
PR	01-SEP-2000; 2000US-0228287P.	
PR	01-SEP-2000; 2000US-0229343P.	
PR	01-SEP-2000; 2000US-0229344P.	
PR	05-SEP-2000; 2000US-0229509P.	
PR	06-SEP-2000; 2000US-0229513P.	
PR	06-SEP-2000; 2000US-0230437P.	
PR	06-SEP-2000; 2000US-0230438P.	
PR	08-SEP-2000; 2000US-0231242P.	
PR	08-SEP-2000; 2000US-0231243P.	
PR	08-SEP-2000; 2000US-0231244P.	
PR	08-SEP-2000; 2000US-0231413P.	
PR	08-SEP-2000; 2000US-0231414P.	
PR	08-SEP-2000; 2000US-0232081P.	
PR	08-SEP-2000; 2000US-0232080P.	
PR	12-SEP-2000; 2000US-0231968P.	
PR	14-SEP-2000; 2000US-0232397P.	
PR	14-SEP-2000; 2000US-0232398P.	
PR	14-SEP-2000; 2000US-0232399P.	
PR	14-SEP-2000; 2000US-0232400P.	
PR	14-SEP-2000; 2000US-0232401P.	
PR	14-SEP-2000; 2000US-0233063P.	
PR	14-SEP-2000; 2000US-0233064P.	
PR	14-SEP-2000; 2000US-0233065P.	
PR	21-SEP-2000; 2000US-0234223P.	
PR	21-SEP-2000; 2000US-0234274P.	
PR	25-SEP-2000; 2000US-0234597P.	
PR	25-SEP-2000; 2000US-0234598P.	

PT renal disorders.

Claim 1; SEQ ID NO 14; 402pp; English.

The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Epstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention.

SQ Sequence 2446 BP; 515 A; 666 C; 700 G; 562 T; 0 U; 3 Other;

Query Match 98.9%; Score 2330.8; DB 8; Length 2446;

Query Match 98.9%; Score 2330.8; DB 8; Length 2446;
Best Local Similarity 99.8%; Pred. No. 0;

Matches 2351; Conservative 3; Mismatches 0; Indels 2; Gaps 2;

QY 1 ATCTTGGCGCCACAGTCGGCCACCGGGGCTCGCGCGCTATGAGAGCGGAGGGGGGC 60

db

[illegible]

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CGTGGGCTGTTGGTCACGGCGCCCCGTACT

142 CCTCGCTGIGCCAGTTTCATCCTCCTGGGACACCACCTCTGTGGTCACCGCGGCCCTGTACT 201

121 CCGTGACCGGCAGAAAGGCCGGGTCTCCCAAGAGCTCAAGGGAGCTAAAAAGTTCAATT 180

Db
202 CCGTGTACCGGAGAGGCCCGGTCTCCCAAGAGCTCAAGGGAGCTAAAAAGTTCA 261

Qy
181 TGGTGAAGATTTAAAGAGTATCTTTCAGAAGCTCCAGGAAATCGGTGCCTTATGCTG 240

Dbb 262 TGGGTGAAGATTAAAGAGTATTCCTTCAGAAGCTCAGGAAAAATGCGTGCGCTTATGCGT 321

QY 241 TTATAGAAGGAGCTGTGCGGTCTGTTAAGAAACGCTTAAACACCACTTTCTCCAAAC

[illegible]

22 44ATGAGAGACGTGGCGTCGTAAAGAAACGCTTAACAGCCAGTTTGTGGAACCT 381

301 GCAAGGGGGTAATTTCAGCGGCTGACACTTCAGGAGCACAAGATGGTGTGGAATCGAACCA 360

db 382 GCAAGGGGTAATTTCAGGGGTGACATTTCAGGAGCACAGATGGTGTGGAATCGACCA 441

QY 361 CCCACCTTTGGGAATGATTGCTCAAAGATCATTTTCATCAGAGGACCAACACAGTGCCTTTG 420

Db
442 CCCACCTTTGGAATGATTGCTCAAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG 501

QY 421 ACCTGGTGCCCCACGAGGATGGCGTGGATGTGGCTGTGCGAGTGCTCAAGGCCCTTGGACT 480

Db

[illegible]

5' CAGTGGGATCTGGGCTCAGAGACTGTATGAGAAGTTCCACCCCCTCGATTCAAGTCCTTCA 3'

562 CAGTGGATCTGGGTCTAGAGACTGTGTATGAGAAGTTCACCCCTCGATTTCAGTCCTTCA 621

541 CCGATGTCATCGGCCCACTACATCAGCGGTGAGCGGCCCAAGGCATCCAAGAGACCGAGG 600

db
622 CCGATGTCATCGGGCCACTACATCAGCGTGAGGGCCAAAGGCATCCAGAGACCGAGG 681

601 AGATGCTGAAGGTGGGGCCACCCTCAGGGGTGGCGAACTGTCCTGGACAACAACT 660

db

682 AGATGCTGAAGTGGGGGCAACCTTCA CAGGGGKTGGGCACTGGTCTCTGCAACACCT

661 CTGTCGGCTGCAGCCCCCGAAAACATCCCAATTGAAACAATCATTTT
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742 CIGTCGCTGCAGCGCCGCAAGGCAATGCAGTACTATCTAAGCAGCCAGGACTTCG 801

QY	721	ACAGCCTGCTGCAGAGGCAGGAGTCCAGCGTCAGGCTCTGGAAGTGTCTGGCGCTGGTTT	780
Db	802	ACAGCCTGCTGCAGAGGCAGGAGTCCAGCGTCAGGCTCTGGAAGTGTCTGGCGCTGGTTT	861
QY	781	TTGGCTTTTGCCACATGTGCCCACCTCTTTCTTCATTTCTCGGAAGCAGTATCTGCAGCGC	840
Db	862	TTGGCTTTTGCCACATGTGCCCACCTCTTTCTTCATTTCTCGGAAGCAGTATCTGCAGCGC	921
QY	841	AGGAGCGCTTCGGCTCAAGCAGATGCAGGAGGAGTCCAGGAGCATGAGGCCAGCTGC	900
Db	922	AGGAGCGCTTCGGCTCAAGCAGATGCAGGAGGAGTCCAGGAGCATGAGGCCAGCTGC	981
QY	901	TGAGCCGACCAAGCCTTGAGGACAGGAGAGTCTGAAGAGCGCCTGTGTAGTGTCTCTGA	960
Db	982	TGAGCCGACCAAGCCTTGAGGACAGGAGAGTCTGAAGAGCGCCTGTGTAGTGTCTCTGA	1041
QY	961	GCAGCTTCAAGTCTTGCGTCTTTCTGAGAGTGTGGGCAGTTTGTTCCTGCACCGAGTGT	1020
Db	1042	GCAGCTTCAAGTCTTGCGTCTTTCTGAGAGTGTGGGCAGTTTGTTCCTGCACCGAGTGT	1101
QY	1021	ACCGCGCTTCGCCAGAGCCCAAGAAGTGCCTATCTCGACACAGCGCATCACCCGGGTGA	1080
Db	1102	ACCGCGCTTCGCCAGAGCCCAAGAAGTGCCTATCTCGACACAGCGCATCACCCGGGTGA	1161
QY	1081	TACCCCTGTACAACAGCTAATAGTTTGGAGCCGCACAGCTTGACCTTGGAAAGCACCCCTG	1140
Db	1162	TACCCCTGTACAACAGCTAATAGTTTGGAGCCGCACAGCTTGACCTTGGAAAGCACCCCTG	1221
QY	1141	CCCCCTTTTCAAGGATTTTTATCTCGAGGCTTTTGGAGGACGAGTGTGTGGGGTAGCTGT	1200
Db	1222	CCCCCTTTTCAAGGATTTTTATCTCGAGGCTTTTGGAGGACGAGTGTGTGGGGTAGCTGT	1281
QY	1201	CACCTCCAGGTATCATTTAGGGAGGAATTGGGTAGAACTCTCCAGACCCTAGCTCCAA	1260
Db	1282	CACCTCCAGGTATCATTTAGGGAGGAATTGGGTAGAACTCTCCAGACCCTAGCTCCAA	1341
QY	1261	TGGCAGGATGCTGCCTTTCCCACTGAGAGGGGACCTGTCCATGTGCAGCCTCATCAGA	1320
Db	1342	TGGCAGGATGCTGCCTTTCCCACTGAGAGGGGACCTGTCCATGTGCAGCCTCATCAGA	1401
QY	1321	GCCTCACCTTGGAGGATGCCGTGGGTCTCTCCAGGAGCCAGATCATGTGCGAGTGTG	1380
Db	1402	GCCTCACCTTGGAGGATGCCGTGGGTCTCTCCAGGAGCCAGATCATGTGCGAGTGTG	1461
QY	1381	ACTGAAATGCCCTATCATCTTAAGCAACCAAGCCAGTGATCAGCAGCTCTTCTGTTCTG	1440
Db	1462	ACTGAAATGCCCTATCATCTTAAGCAACCAAGCCAGTGATCAGCAGCTCTTCTGTTCTG	1521
QY	1441	TGCTCTTCTGTTTTTTCTGGTGAATCGTTGCTTGTGTCAGTGTGGAGGACTCAGAG	1500
Db	1522	TGCTCTTCTGTTTTTTCTGGTGAATCGTTGCTTGTGTCAGTGTGGAGGACTCAGAG	1580
QY	1501	GGGAGAAAGGCTGGGCCCGCAGTACAACGGATGCTTGGGTGCTGCCTCCGAAGAGACT	1560
Db	1581	GGGAGAAAGGCTGGGCCCGCAGTACAACGGATGCTTGGGTGCTGCCTCCGAAGAGACT	1640
QY	1561	CTCCCGCAGCTTTCTTCTTTTCTCTCATGCCCGGGAAACAGTCTTCTTCAGAAATGTT	1620
Db	1641	CTCCCGCAGCTTTCTTCTTTTCTCTCATGCCCGGGKAAACAGTCTTCTTCAGAAATGTT	1700
QY	1621	CAGGCTGGGCAGGTCAACTTGTGTTCTTTTCCCTTCACCTGCTGCCTCTTAAAGCCTG	1680
Db	1701	CAGGCTGGGCAGGTCAACTTGTGTTCTTTTCCCTTCACCTGCTGCCTCTTAAAGCCTG	1760
QY	1681	CAGTGTGTGTAGGACAAAAAGTAGTGAAGTTCAGCATATCCGCTTCTGCCAGATGTT	1740
Db	1761	CAGTGTGTGTAGGACAAAAAGTAGTGAAGTTCAGCATATCCGCTTCTGCCAGATGTT	1820
QY	1741	CGGGGCCCCGGCCACAGATTCAGAGAGATCATGTGAAGGGCAGTGTGTGTCAGGCACC	1800
Db	1821	CGGGGCCCCGGCCACAGATTCAGAGAGATCATGTGAAGGGCAGTGTGTGTCAGGCACC	1880

AA
DR WPI; 2002-292408/33.
DR P-PSDB: ABB97404.

XX	An isolated polynucleotide for treating diseases associated with its
PT	encoded polypeptide such as cancer and multiple sclerosis.
XX	Claim 1; SEQ ID NO 228; 509pp; English.
XX	The present invention provides the protein and coding sequences of 444
CC	novel human proteins. These were isolated from expressed sequences tags
CC	(ESTs). They can be used to stimulate cell growth, to regulate
CC	haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC	e.g. in burn treatment, to regulate the immune system e.g. to treat
CC	multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC	infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
CC	and cancer, to screen for drugs, to treat inflammatory conditions e.g.
CC	rheumatoid arthritis, and to treat nervous system disorders e.g. of the
CC	Parkinson's disease. The present sequence is a coding sequence of the
XX	invention
XX	Sequence 2717 BP; 554 A; 754 C; 794 G; 614 T; 0 U; 1 Other;
SQ	
	Query Match 97.3%; Score 2291.8; DB 6; Length 2717;
	Best Local Similarity 98.9%; Pred. No. 0;
	Matches 2327; Conservative 0; Mismatches 23; Indels 2; Gaps 2;
QY	1 ATCTTGGCGGCACAGTCGCGCCACCGGGGTCCGCCGTCATGGAGCGAGGCGCGC 60
DB	368 ATCTTGGCGGCACAGTCGCGCCACCGGGGTCCGCCGTCATGGAGCGAGGCGCGC 427
QY	61 CCTCGCTGTGCGAGTTCACTCTCTGCGGCACCACCTCTGTGGTCACCGCCGCTGTACT 120
DB	428 CCTCGCTGTGCGAGTTCACTCTCTGCGGCACCACCTCTGTGGTCACCGCCGCTGTACT 487
QY	121 CCGTGTAACCGCAGAAAGCCCGGGTCTCCGAAGAGCTCAAGGAGCTTAAAAAGTTCA TT 180
DB	488 CCGTGTAACCGCAGAAAGCCCGGGTCTCCGAAGAGCTCAAGGAGCTTAAAAAGTTCA TT 547
QY	181 TGGGTGAAGATTAAAGAGTATCTTTTCAGAAGCTCCAGGAATAATGGTGCTTATGCTG 240
DB	548 TGGGTGAAGATTAAAGAGTATCTTTTCAGAAGCTCCAGGAATAATGGTGCTTATGCTG 607
QY	241 TTATAGAAGGAGCTGTGCGGTCTCTTAAAGAAAAGCTTAAACAGCCAGTTGTGGAAAAC T 300
DB	608 TTATAGAAGGAGCTGTGCGGTCTCTTAAAGAAAAGCTTAAACAGCCAGTTGTGGAAAAC T 667
QY	301 GCAAGGGGGTAATTACGGGGTGACACTTTCAGGAGACAAGATGGTGTGGAAATCGAACCA 360
DB	668 GCAAGGGGGTAATTACGGGGTGACACTTTCAGGAGACAAGATGGTGTGGAAATCGAACCA 727
QY	361 CCCACCTTTGGAAATGATTGTCTCAAAGATCATTCAGAGACCAACACAGTCGCGCTTTG 420
DB	728 CCCACCTTTGGAAATGATTGTCTCAAAGATCATTCATCAGAGACCAACACAGTCGCGCTTTG 787
QY	421 ACCTGGTCCCCACAGAGATGGCGTGAATGTGGCTGTGCGAGTGTGGAAGCCCTTGGACT 480
DB	788 ACCTGGTCCCCACAGAGATGGCGTGAATGTGGCTGTGCGAGTGTGGAAGCCCTTGGACT 847
QY	481 CAGTGGATCTGGGTCTAGAGACTGTGTATGAAAGTTCCAACCCCTCGAATTCAGTCTTCA 540
DB	848 CAGTGGATCTGGGTCTAGAGACTGTGTATGAAAGTTCCAACCCCTCGAATTCAGTCTTCA 907
QY	541 CCGATGTCTATCGGCCACTACATCACGGGTGACGCGCCCAAGGATCCAAAGAGACCGAGG 600
DB	908 CCGATGTCTATCGGCCACTACATCACGGGTGACGCGCCCAAGGATCCAAAGAGACCGAGG 967
QY	601 AGATGCTGAAGTGGGGGCCACCCCTCACAGGGGTTGGGAACTGGTCTCTGGCAACAACCT 660
DB	968 AGATGCTGAAGTGGGGGCCACCCCTCACAGGGGTTGGGAACTGGTCTCTGGCAACAACCT 102
QY	661 CTGTCCGCTGCAGCGGCCCAACAAAGGATTCAGATCTATCTTAGCAGCCAGGACTTCG 720
DB	1028 CTGTCCGCTGCAGCGGCCCAACAAAGGATTCAGATCTATCTTAGCAGCCAGGACTTCG 108
QY	721 ACAGCCTGTGCAGAGCGAGGAGTCGAGCGTCTGGAAAGGTGTGGCGCTGGTTT 780

[illegible]

Db	2168	TCCTGGTTTCGCCACTGGCCCTGATTTTGA	CTCTGCACTTGGGAGAGCTCGGGTGGT	2222
QY	1861	CCCTCGTTTTCCTCCTCGGAAATGAGCGCAGAGGCTCGCTCTCTGAAAGGACGAGTG	1920	
Db	2228	CCCTCGTTTTCCTCCTCGGAAATGAGCGCAGAGGCTCGCTCTCTGAAAGGACGAGTG	2286	
QY	1921	TGGATGCCACTGGGCTAGTGTCCTGGGCTCACAGCTTCCTTGAAGGCTGTCAACAGGAA	1980	
Db	2287	TGGATGCCACTGGGCTAGTGTCCTGGGCTCACAGCTTCCTTGAAGGCTGTCAACAGGAA	2346	
QY	1981	AAGCAGCGGCTGCGACCTGAGCATATGCCCTCTTGGGGCTCCCTCATCCAGCCCGTCG	2040	
Db	2347	AAGCAGCGGNTGCGACCTGAGCATATGCCCTTGGGGCTCCCTCATCCAGCCCGTCG	2406	
QY	2041	CAGCTTTGACATCTTTGGTGTA	CTCATGCTTCCTTGTGTACCCCTCCAGTATT	2100
Db	2407	CAGCTTTGACATCTTTGGTGTA	CTCATGCTTCCTTGTGTACCCCTCCAGTATT	2465
QY	2101	ACCATTGGCCCTCACCTGCCCTTGGTGAGCCTTTTAGTGCAAGACAGATGGGGCTGTTT	2160	
Db	2466	ACCATTGGCCCTCACCTGCCCTTGGTGAGCCTTTTAGTGCAAGACAGATGGGGCTGTTT	2525	
QY	2161	TCCGCCACCTCTGAGTAGTGGAGGTCA	CATACACAGCTCTTTTTTATTGCCCCTTTCT	2220
Db	2526	TCCGCCACCTCTGAGTAGTGGAGGTCA	CATACACAGCTCTTTTTTATTGCCCCTTTCT	2585
QY	2221	GCCTCTGAATGTTTCATCTCTCGCTCCCTTGGTGAGGCGAGGAAGGGTGCCCTCAGGG	2280	
Db	2586	GCCTCTGAATGTTTCATCTCTCGCTCCCTTGGTGAGGCGAGGAAGGGTGCCCTCAGGG	2645	
QY	2281	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC	2340	
Db	2646	GCCGACACTAGTATGATGCAGTGTCCAGTGTGAACAGCAGAAATTAACATGTTGCAACC	2705	
QY	2341	AAAAAAAAAAAA	2352	
Db	2706	AAAAAAAAAAAA	2717	
RESULT 12				
ABAB2998				
ID	ABA82998 standard; DNA; 2377 BP.			
XX	ABA82998;			
XX	05-FEB-2002 (first entry)			
DT	Human transcription factor TRFX-25 coding sequence.			
DE	Human; transcription factor; TRFX; cell proliferative disease;			
KW	autoimmune disease; inflammation; neurological disease; chromosome 1;			
KW	developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;			
KW	neuroprotective; antiinflammatory; gene therapy; ds.			
XX	Homo sapiens.			
OS	WO200172777-A2.			
PN	04-OCT-2001.			
PD	13-MAR-2001; 2001WO-US008117.			
XX	13-MAR-2000; 2000US-0188986P.			
PR	(INCY-) INCYTE GENOMICS INC.			
XX	Hillman JL, Baughn MR, Yue H, Lal P, Lu DM, Patterson C;			
PI	Azimzai Y, Bandman O, Tang Yi, Mathur P, Shah P, Au-Young J;			
PI	Reddy R,			
XX	WPI; 2001-570896/64.			
DR	P-PSDB; ABB50174.			
XX				

PT Novel transcription factor polypeptides, used to treat diseases
 PT associated with altered activity and expression of TRFX, and to screen
 PT for agents capable of modulating its activity.
 XX PS Claim 11; Page 271; 327pp; English.

XX The present sequence is the coding sequence for a human transcription
 CC factor. The transcription factor and its coding sequence are useful in
 CC the diagnosis, treatment and prevention of diseases associated with
 CC altered expression of the transcription factor e.g. cell proliferative,
 CC autoimmune/inflammatory, neurological and developmental disorders. A
 CC number of specific disorders/diseases are given in the specification,
 CC including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,
 CC allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic
 CC dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,
 CC Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,
 CC psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative
 CC colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's
 CC disease, stroke, and viral, bacterial, fungal and protozoal infections.
 CC The present sequence maps to human chromosome 1

XX SQ Sequence 2377 BP; 494 A; 652 C; 683 G; 548 T; 0 U; 0 Other:

Query Match 94.1%; Score 2217; DB 5; Length 2377;
 Best Local Similarity 97.9%; Pred. No. 0;
 Matches 2304; Conservative 0; Mismatches 5; Indels 44; Gaps 4;

QY 1 ATCTTGGGCCACAGTCGCGCCACCGGGCTCGCGCGCTCATGGAGCGAGGGCGGC 60
 DB 68 ATCTTGGGCCACAGTCGCGCCACCGGGCTCGCGCGCTCATGGAGCGAGGGCGGC 127
 QY 61 CCTCGCTGTGCCAGTTCATCCTCTCTGGGCACCACTCTGTGGTACCGCGCGCTGTACT 120
 DB 128 CCTCGCTGTGCCAGTTCATCCTCTCTGGGCACCACTCTGTGGTACCGCGCGCTGTACT 187
 QY 121 CCGTGTAACGGGAGAGCGCGGTCTCCCAAGAGCTCAAGGGAGCTAAAGAGTTTCATT 180
 DB 188 CCGTGTAACGGGAGAGCGCGGTCTCCCAAGAGCTCAAGGGAGCTAAAGAGTTTCATT 247
 QY 181 TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCGTGTATGCTG 240
 DB 248 TGGGTGAAGATTAAAGAGTATCTTTTCAAGAGCTCCAGGAAATGCGTGTATGCTG 307
 QY 241 TTATAGAAGAGCTGTGCGTCTGTAAAGAAAGCTTAAACAGCCAGTTTGTGAAACT 300
 DB 308 TTATAGAAGAGCTGTGCGTCTGTAAAGAAAGCTTAAACAGCCAGTTTGTGAAACT 367
 QY 301 GCAAGGGGTAAATTCAGGGGTGACACTTCAGGAGCACAGATGCTGGAATCGAACCA 360
 DB 368 GCAAGGGGTAAATTCAGGGGTGACACTTCAGGAGCACAGATGCTGGAATCGAACCA 427
 QY 361 CCCACCTTTGGAATGATGTCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG 420
 DB 428 CCCACCTTTGGAATGATGTCTCAAGATCATTCATCAGAGGACCAACACAGTGCCTTTG 487
 QY 421 ACCTGGTCCCCCAGAGATGGGTGATGTGGTGTGCGAGTGTGAAGCCCTTGACT 480
 DB 488 ACCTGGTCCCCCAGAGATGGGTGATGTGGTGTGCGAGTGTGAAGCCCTTGACT 547
 QY 481 CAGTGGATCTGGGTCTAGAGCTGTGTATGAGAGTTCACCCCTCGATTTCAGTCTTCA 540
 DB 548 CAGTGGATCTGGGTCTAGAGCTGTGTATGAGAGTTCACCCCTCGATTTCAGTCTTCA 607
 QY 541 CCGATGTCTATCGGCCACCTACATCAGCGGTGAGCGGCCCAAGGCCATCCAGAGACCGAGG 600
 DB 608 CCGATGTCTATCGGCCACCTACATCAGCGGTGAGCGGCCCAAGGCCATCCAGAGACCGAGG 667
 QY 601 AGATGCTGAAGTGGGGGCCACCTTCACAGGGGTTGGCGAATGCTGCTGGACACAACT 660
 DB 668 AGATGCTGAAGTGGGGGCCACCTTCACAGGGGTTGGCGAATGCTGCTGGACACAACT 727
 QY 661 CTGTCCGCTGCAGCGGCCCAAGAGGATCGAGTACTATCTTAAGAGCCAGGACTTCG 720

DB 728 CTGTCCGCTGCAGCGGCCCAAAAGAGCATGACGACTACTATCTAAGAGCCAGGACTTCG 787
 QY 721 ACAGCTCTCTCAGAGGAGGAGTGCAGCTCAGGCTCTGGAAGTGTCTGGCGCTGGTTT 780
 DB 788 ACAGCTCTCTCAGAGGAGGAGTGCAGCTCAGGCTCTGGAAGTGTCTGGCGCTGGTTT 847
 QY 781 TTGGCTTTGCCACATGTGCCCTCTTCTTCAATCTTCCGGAAGCAGTATCTGCGCGGC 840
 DB 848 TTGGCTTTGCCACATGTGCCCTCTTCTTCAATCTTCCGGAAGCAGTATCTGCGCGGC 907
 QY 841 AGAGCGCTGTGCGCTCAAGCAGATGTCAGGAGAGTTCAGGAGCATGAGGCCAGCTGC 900
 DB 908 AGAGCGCTGTGCGCTCAAGCAGATGTCAGGAGAGTTCAGGAGCATGAGGCCAGCTGC 967
 QY 901 TGAGCGGACCAAGCTTGAGGACAGGAGAGTCTGAAGAGCGCTCTGTAGTGTCTGA 960
 DB 968 TGAGCGGACCAAGCTTGAGGACAGGAGAGTCTGAAGAGCGCTCTGTAGTGTCTGA 1027
 QY 961 CGAGCTTCAAGTCTCTGCTCTTCTGAGTGTGGCACCTTTGTTCTGACCCAGTGTCT 1020
 DB 1028 CGAGCTTCAAGTCTCTGCTCTTCTGAGTGTGGCACCTTTGTTCTGACCCAGTGTCT 1087
 QY 1021 ACGCGCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGGTGA 1080
 DB 1088 ACGCGCTTGCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCCGGGTGA 1147
 QY 1081 TACCCCTGTACACAGCTAATAGTTTGAAGCCGCAAGCTTGCACCTGGAAGCACCCCTG 1140
 DB 1148 TACCCCTGTACACAGCTAATAGTTTGAAGCCGCAAGCTTGCACCTGGAAGCACCCCTG 1207
 QY 1141 CCCCCTTTTTCAGGGATTTTATCTCGAGGCTTTTGAAGAGCAGTGTGGGTGAGTGTCT 1200
 DB 1208 CCCCCTTTTTCAGGGATTTTATCTCGAGGCTTTTGAAGAGCAGTGTGGGTGAGTGTCT 1267
 QY 1201 CACCTCAGATATGATGAGGAGGAGTATGGGTAGAACTCTCCAGACCCATGCTCCAA 1260
 DB 1268 CACCTCAGATATGATGAGGAGGAGTATGGGTAGAACTCTCCAGACCCATGCTCCAA 1327
 QY 1261 TGSCAGAGTCTGCTTTCACCTGAGAGGAGACCTGTCCATGTGTCAGCTCATCAGA 1320
 DB 1328 TGSCAGAGTCTGCTTTCACCTGAGAGGAGACCTGTCCATGTGTCAGCTCATCAGA 1387
 QY 1321 GCCTCACCTTGGAGAGTATGCGGTGCGTCTCTCCAGAGGAGGAGTATGAGTGTG 1380
 DB 1388 GCCTCACCTTGGAGAGTATGCGGTGCGTCTCTCCAGAGGAGGAGTATGAGTGTG 1447
 QY 1381 ACTGAAATGCTCATCATTAAGACCAAGAGCAGTATCAGCAGCTCTTCTGTTCTG 1440
 DB 1448 ACTGAAATGCTCATCATTAAGACCAAGAGCAGTATCAGCAGCTCTTCTGTTCTG 1507
 QY 1441 TGTCTTCTGTTTCTTCTGTTGATGTTGCTTCTGTCGTGAGTGTGGTGGAGGACTCAG 1500
 DB 1508 TGTCTTCTGTTTCTTCTGTTGATGTTGCTTCTGTCGTGAGTGTGGTGGAGGACTCAG 1567
 QY 1501 GGGAGGAAAGGCTGGGCGCCGAGTACAAAGGATGCTTGGGTGCTGCTCCGAGAGACT 1560
 DB 1568 GGGAGGAAAGGCTGGGCGCCGAGTACAAAGGATGCTTGGGTGCTGCTCCGAGAGACT 1627
 QY 1561 CTGCGGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1620
 DB 1628 CTGCGGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1687
 QY 1621 CAGCTGGGAGGCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1680
 DB 1688 CAGCTGGGAGGCTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1747
 QY 1681 CACCTGTGTAGAGGACAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1740
 DB 1748 CACCTGTGTAGAGGACAAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1807
 QY 1741 CGGGCCCCGGGCAACAGATGAGAGAGATCATGTGAAGGAGTGTGTCAGGAGGAGCC 1800
 DB 1808 CGGGCCCCGGGCAACAGATGAGAGAGATCATGTGAAGGAGTGTGTCAGGAGGAGCC 1867

Db	661	AGCTGCTGAGCCGAGCCAGACCTGAGGACAGGAGTCTGAAGAGCGCTGTGTAGTGT	720
Qy	955	GTCTGAGCAGCTTCAAGTCTCTGCTTTCTGAGGTGGGACAGTTTGTCTCTGACCG	1014
Db	721	GTCTGAGCAGCTTCAAGTCTCTGCTTTCTGAGGTGGGACAGTTTGTCTCTGACCG	780
Qy	1015	AGTGCTACCGCGCTTCCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCC	1074
Db	781	AGTGCTACCGCGCTTCCAGAGCCCAAGAGTGCCTATCTGCAGACAGGCGATCACCC	840
Qy	1075	GGGTGATACCCCTGTCAACACAGCTAATAGTTTGGAAAGCCGACACAGCTTGACCTGGAAGCA	1134
Db	841	GGGTGATACCCCTGTCAACACAGCTAATAGTTTGGAAAGCCGACACAGCTTGACCTGGAAGCA	900
Qy	1135	CCCTGCGCCCTTTTCAGGAAATTTTATCTCAGAGCCCTTTGAGAGCAGTGGTGGGGT	1194
Db	901	CCCTGCGCCCTTTTCAGGAAATTTTATCTCAGAGCCCTTTGAGAGCAGTGGTGGGGT	960
Qy	1195	AGCTGTCACTCCAGGTATGATGAGGAGGAATTCGGTAGAACTCTCCAGACCCATGC	1254
Db	961	AGCTGTCACTCCAGGTATGATGAGGAGGAATTCGGTAGAACTCTCCAGACCCATGC	1020
Qy	1255	CTCCAAATGGCAGGATGCTGCTTTTCCACCTCAGAGGGGACCCCTGTCCATGTGCAGCCCTC	1314
Db	1021	CTCCAAATGGCAGGATGCTGCTTTTCCACCTCAGAGGGGACCCCTGTCCATGTGCAGCCCTC	1080
Qy	1315	ATCAGAGCTCACCCCTGGGAGTAGCCGTGGCGTCTCTCCAGAGGACCCAGATCAGTGGG	1374
Db	1081	ATCAGAGCTCACCCCTGGGAGTAGCCGTGGCGTCTCTCCAGAGGACCCAGATCAGTGGG	1140
Qy	1375	AGTGTGACTGAAATGCGTCACTTAAGCACCAGCCAGTGATCAGCAGCTCTCTCG	1434
Db	1141	AGTGTGACTGAAATGCGTCACTTAAGCACCAGCCAGTGATCAGCAGCTCTCTCTCG	1200
Qy	1435	TTCCCTGTCTCTGTTTTTTCTGCTGTAATGCTGTCTCTGGAATTTGGTGGAGGAC	1494
Db	1201	TTCCCTGTCTCTGTTTTTTCTGCTGTAATGCTGTCTCTGGAATTTGGTGGAGGAC	1260
Qy	1495	TCAGAGGGGAGAAAGGTGGGCCCCGAGTCAACCGATCCCTTGGGTGCTGCTCCGAA	1554
Db	1261	TCAGAGGGGAGAAAGGTGGGCCCCGAGTCAACCGATCCCTTGGGTGCTGCTCCGAA	1320
Qy	1555	GAGACTCTGCGCAGCTTTCTTTCTTTCTATGCCCCGGGAAACAGTCTTCTTCAG	1614
Db	1321	GAGACTCTGCGCAGCTTTCTTTCTTTCTATGCCCCGGGAAACAGTCTTCTTCAG	1380
Qy	1615	AATTTGTAGGCTGGGACGTCACCTGTGTTCTTTTCCCTCTCAGCTCTGCTTCCCTTAA	1674
Db	1381	AATTTGTAGGCTGGGACGTCACCTGTGTTCTTTTCCCTCTCAGCTCTGCTTCCCTTAA	1440
Qy	1675	CGCCTGCACTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACATCCGCTCTGCCCCA	1734
Db	1441	CGCCTGCACTGTGTGTAGAGGACAAAGAAAGTGAAGTCAGACATCCGCTCTGCCCCA	1500
Qy	1735	GATGTGTGGGGCCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTTGGTCAGG	1794
Db	1501	GATGTGTGGGGCCCCCGGGCAACAGATTGAAGAGATCATGTGAAGGCGAGTTGGTCAGG	1560
Qy	1795	CAGGCTCTGCTGTTTCCGCACTGGCCCTGATTGTAACCTCTGCGCACTGGGAGAGCTCGG	1854
Db	1561	CAGGCTCTGCTGTTTCCGCACTGGCCCTGATTGTAACCTCTGCGCACTGGGAGAGCTCGG	1581
Qy	1855	GGTGTGCTCTGTTTTTCCCTCTCTGAGAAATGAGGCGCAGAGGCTCTGCTCTGAAGGAC	1914
Db	1582	--TGGTCCCTGGTTTCTCTCTCTGAGAAATGAGGCGCAGAGGCTCTGCTCTGAAGGAC	1639
Qy	1915	GCAGTGTGATGCACTGGCCCTAGTGTCTGGCTCAGAGCTTCTTGCAGAGGCTGTAC	1974
Db	1640	GCAGTGTGATGCACTGGCCCTAGTGTCTGGCTCAGAGCTTCTTGCAGAGGCTGTAC	1699
Qy	1975	AGGGAAGACAGCGCGCTGGCACTCTGAGCATATCCCTCTTGGGGCTCCCTCATCCAGC	2034

PR	14-AUG-2000;	2000US-0224518P.	PR	08-NOV-2000;	2000US-0246477P.
PR	14-AUG-2000;	2000US-0224519P.	PR	08-NOV-2000;	2000US-0246478P.
PR	14-AUG-2000;	2000US-0225213P.	PR	08-NOV-2000;	2000US-0246524P.
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PR	01-SEP-2000;	2000US-0229345P.	PR	17-NOV-2000;	2000US-0249215P.
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PR	14-SEP-2000;	2000US-0232397P.	PR	05-DEC-2000;	2000US-0251030P.
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PR	14-SEP-2000;	2000US-0233359P.	PR	06-DEC-2000;	2000US-0256719P.
PR	14-SEP-2000;	2000US-0232400P.	PR	08-DEC-2000;	2000US-0251479P.
PR	14-SEP-2000;	2000US-0232401P.	PR	08-DEC-2000;	2000US-0251856P.
PR	14-SEP-2000;	2000US-0233063P.	PR	08-DEC-2000;	2000US-0251868P.
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PR	14-SEP-2000;	2000US-0233065P.	PR	08-DEC-2000;	2000US-0251899P.
PR	21-SEP-2000;	2000US-0234223P.	PR	08-DEC-2000;	2000US-0251990P.
PR	21-SEP-2000;	2000US-0234374P.	PR	11-DEC-2000;	2000US-0254037P.
PR	25-SEP-2000;	2000US-0234997P.	PR	05-JAN-2001;	2001US-0259678P.
PR	26-SEP-2000;	2000US-0234998P.	PR		
PR	26-SEP-2000;	2000US-0235484P.	PR	(HUMA-) HUMAN GENOME SCI INC.	
PR	27-SEP-2000;	2000US-0235834P.	PR	Rosen CA, Barash SC, Ruben SM;	
PR	27-SEP-2000;	2000US-0235836P.	PR	WPI, 2001-488783/53.	
PR	29-SEP-2000;	2000US-0236327P.	PR	P-PSDB; AAU16309.	
PR	29-SEP-2000;	2000US-0236367P.	PR	New nucleic acid molecules encoding 461 human secreted proteins for	

CC and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed

Query Match		75.0%;	Score 1766;	DB 4;	Length 1791;
Best Local Similarity		99.8%;	Pred. No. 0;		
Matches 1774;		Conservative	5;	Mismatches	1; Gaps 1;
QY	576	CCCAAGGATCAAGAGACCGAGGAGATGCTGAAGGTGGGGCCACCTTCACAGGGTT	635		
DB	1	CCCAAGGCATCAAGAGACCGAGGAGATGCTGAAGGTGGGGCCACCTTCACAGGGTT	60		
QY	636	GGCGAACTGCTCTGAGCAACAACCTGTGTCGGCTGCGAGCGGCCCAAGAGCATGCAG	695		
DB	61	GGCGAACTGCTCTGAGCAACAACCTGTGTCGGCTGCGAGCGGCCCAAGAGCATGCAG	120		
QY	696	TACTATCTAAGCAGCAGGACTTCGACAGCTGTGTCAGAGCGAGGAGTCGAGCTCAGG	755		
DB	121	TACTATCTAAGCAGCAGGACTTCGACAGCTGTGTCAGAGCGAGGAGTCGAGGTCAGG	180		
QY	756	CTCTGAAGGTGCTGGCGCTGGTTTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATT	815		
DB	181	CTCTGAAGGTGCTGGCGCTGGTTTTTGGCTTTGCCACATGTGCCACCTCTTCTTCATT	240		
QY	816	CTCCGGAAGCAGATATCTGACGCGCAGAGGCGCTGCGCTCAAGCAGATGCAGGAGG	875		
DB	241	CTCCGGAAGCAGATATCTGACGCGCAGAGGCGCTGCGCTCAAGCAGATGCAGGAGG	300		
QY	876	TTCCAGGAGCATGAGGCGCAGCTCTGAGCGGAGCCCAAGCTGAGGACAGGAGAGTCTG	935		
DB	301	TTCCAGGAGCATGAGGCGCAGCTCTGAGCGGAGCCCAAGCTGAGGACAGGAGAGTCTG	360		
QY	936	AAGAGCGCCTGTGTAGTGTGTCTGAGCAGCTTCAAGTCTGCGCTTTCTGGAGTGTGG	995		
DB	361	AAGAGCGCCTGTGTAGTGTGTCTGAGCAGCTTCAAGTCTGCGCTTTCTGGAGTGTGG	420		
QY	996	CACGTTTGTCTGCAACGAGTGTACCGCGCTTGCAGAGCCCAAGAGTGCCTTATC	1055		
DB	421	CACGTTTGTCTGCAACGAGTGTACCGCGCTTGCAGAGCCCAAGAGTGCCTTATC	480		
QY	1056	TGCAGACAGCGCATCACCGGCTGATACCCCTGTACACAGCTAATAGTTTGGAGCGGC	1115		
DB	481	TGCAGACAGCGCATCACCGGCTGATACCCCTGTACACAGCTAATAGTTTGGAGCGGC	540		
QY	1116	ACAGCTTGACCTGGAAGCACCCCTGCCCCCTTTTTCAGGATTTTATCTCGAGGCTTTG	1175		
DB	541	ACAGCTTGACCTGGAAGCACCCCTGCCCCCTTTTTCAGGATTTTATCTCGAGGCTTTG	600		
QY	1176	GAGAGCAGTGTGGGGTACTGTACCTCAGGTATGATTGAGGGGAAATTTGGGTAG	1235		
DB	601	GAGAGCAGTGTGGGGTACTGTACCTCAGGTATGATTGAGGGGAAATTTGGGTAG	660		
QY	1236	AAACTCTCCAGACCATGCTCCAAATGGCAGGATGCTGCCCTTTCACCTCAGAGGGGAC	1295		
DB	661	AAACTCTCCAGACCATGCTCCAAATGGCAGGATGCTGCCCTTTCACCTCAGAGGGGAC	720		
QY	1296	CCTGTCCATGTGCAGCTCATCAGAGCTCACCTTGGGAGGATGCCGTGGCTCTCTCC	1355		
DB	721	CCTGTCCATGTGCAGCTCATCAGAGCTCACCTTGGGAGGATGCCGTGGCTCTCTCC	780		
QY	1356	CAGAGCCAGATCAGTGCAGTGTGACTGAAATGCGCTCATCATTAAAGCACAAGCCA	1415		
DB	781	CAGAGCCAGATCAGTGCAGTGTGACTGAAATGCGCTCATCATTAAAGCACAAGCCA	840		
QY	1416	GTGATCAGCAGCTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTGTCTGTCTGTCTGT	1475		

DB	841	GTGATCAGCAGCTCTTCTGTCTTCTGTCTTCTGTCTTCTGTCTGTCTGTCTGTCTGT	900		
QY	1476	TGTGACCTTGTGTGAGGACTCAGAGGGAGGAAAGGCTCGGCCCGAGTACAACGATGC	1535		
DB	901	TGTGACCTTGTGTGAGGACTCAGAGGGAGGAAAGGCTCGGCCCGAGTACAACGATGC	960		
QY	1536	CTTGGTGTGTCTCGAAGAGACTCTGCCGAGCTTTTCTTCTTTTCTTCTTCTTCTTCT	1595		
DB	961	CTTGGTGTGTCTCGAAGAGACTCTGCCGAGCTTTTCTTCTTTTCTTCTTCTTCTTCT	1020		
QY	1596	GGAAACAGCTTTTCTTCAAAATGTGAGGTGGGAGGTCAACTGTGTCTTCTTCTTCT	1655		
DB	1021	GGAAACAGCTTTTCTTCAAAATGTGAGGTGGGAGGTCAACTGTGTCTTCTTCTTCT	1080		
QY	1656	CACCTGCTTGCCTTCAACGCTGCACTGTGTGTAGAGGACAAAGAAAGTGAAGTCA	1715		
DB	1081	CACCTGCTTGCCTTCAACGCTGCACTGTGTGTAGAGGACAAAGAAAGTGAAGTCA	1140		
QY	1716	GCACATCCGCTTCTGCCAGATGCTCGGGGCCCGGGCCCAACAGATTGAAGAGAGATCATG	1775		
DB	1141	GCACATCCGCTTCTGCCAGATGCTCGGGGCCCGGGCCCAACAGATTGAAGAGAGATCATG	1200		
QY	1776	TGAAGGCGAGTGTGTGAGGAGGCTCTGTGTTCGGCTTTCGGCTTTCGGCTTTCGGCT	1835		
DB	1201	TGAAGGCGAGTGTGTGAGGAGGCTCTGTGTTCGGCTTTCGGCTTTCGGCTTTCGGCT	1260		
QY	1836	GCCACTTGGGAGAGCTCGGGGTGCTCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCT	1895		
DB	1261	GCCACTTGGGAGAGCTCGGGGTGCTCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCT	1320		
QY	1896	GCCTCGCTTCTTGAAGGAGCAGCTGTGGATGCCATCTGGCTTCTTCTTCTTCTTCTTCT	1955		
DB	1321	GCCTCGCTTCTTGAAGGAGCAGCTGTGGATGCCATCTGGCTTCTTCTTCTTCTTCTTCT	1380		
QY	1956	TTCTTGAAGGCTGTCAAAAGGAAAGCAGCGGCTGGCACCTTGAGCATATGCCCTCT	2015		
DB	1381	TTCTTGAAGGCTGTCAAAAGGAAAGCAGCGGCTGGCACCTTGAGCATATGCCCTCT	1440		
QY	2016	TGGGGCTTCTTCAACGCGCTTGCAGCTTTCACATCTTGGTGTACTCATGTGCTTCT	2075		
DB	1441	TGGGGCTTCTTCAACGCGCTTGCAGCTTTCACATCTTGGTGTACTCATGTGCTTCT	1500		
QY	2076	CTTGTGTATACCCCTTCCAGATTAACATTTGCCCTTCCCTTCTTCTTCTTCTTCTTCT	2135		
DB	1501	CTTGTGTATACCCCTTCCAGATTAACATTTGCCCTTCCCTTCTTCTTCTTCTTCTTCT	1560		
QY	2136	TAGTGAAGCAGATGGGGCTGTTTTCCCGACCTCTGAGTAGTGTGAGGTCAATACAC	2195		
DB	1561	TAGTGAAGCAGATGGGGCTGTTTTCCCGACCTCTGAGTAGTGTGAGGTCAATACAC	1620		
QY	2196	AGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	2255		
DB	1621	AGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1680		
QY	2256	AGGCGAAGAGGGGTGCTTCCAGGGCGACACTAGTAGTATGATGAGTGTCCAGTGTGAC	2315		
DB	1681	AGGCGAAGAGGGGTGCTTCCAGGGCGACACTAGTAGTATGATGAGTGTCCAGTGTGAC	2356		
QY	2316	AGCAGAAATTAACATGTTGCAACCAAAAAAAAAAAAAAAAAAAAAA	2356		
DB	1740	AGCAGAAATTAACATGTTGCAACCAAAAAAAAAAAAAAAAAAAAAA	1780		

RESULT 15
ABX73637
ID ABX73637 standard; DNA; 1791 BP.
XX
AC ABX73637;
XX
DT 18-MAR-2003 (first entry)
XX
DE Human novel polynucleotide #465.
XX

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us-09-978-360a-32.rng

Db 601 GAGGAGCAGTGGTGGGGTAGCTGTCACTCCAGGTATGATGAGGAGGAATTTGGGTAG 660
QY 1236 AAACCTCCAGACCCATGCTCAATGGCAGGATGCTGCCTTTCCACCTGAGAGGGGAC 1295
Db 661 AAACCTCCAGACCCATGCTCAATGGCAGGATGCTGCCTTTCCACCTGAGAGGGGAC 720
QY 1296 CCTGTCCATGTGACGCTCATCAGAGCTCAACCTGGAGGATGCCGTGGGTCTCTCC 1355
Db 721 CCTGTCCATGTGACGCTCATCAGAGCTCAACCTGGAGGATGCCGTGGGTCTCTCC 780
QY 1356 CAGAGCCAGATCAGTGGAGTGTGACTGAATAATGCTCATCTAAGCACCAAGCCA 1415
Db 781 CAGAGCCAGATCAGTGGAGTGTGACTGAATAATGCTCATCTAAGCACCAAGCCA 840
QY 1416 GTGATCAGCAGCTCTCTGTTCCTGTGCTCTCTGTTCCTGTTCCTGTTCCTGTTC 1475
Db 841 GTGATCAGCAGCTCTCTGTTCCTGTGCTCTCTGTTCCTGTTCCTGTTCCTGTTC 900
QY 1476 TGTGGACTTGTGGAGGACTCAGAGGGAGGAAAGGCTGGGCCCGGAGTACACGGATGC 1535
Db 901 TGTGGACTTGTGGAGGACTCANAGGGAGGAAAGGCTGGGCCCGGAGTACACGGATGC 960
QY 1536 CTGGGTGCTGCTCCGAGAGACTCTGCCGAGCTTTCTCTTTTCTCTCATGCCCCG 1595
Db 961 CTGGGTGCTGCTCCGAGAGACTCTGCCGAGCTTTCTCTTTTCTCTCATGCCCCG 1020
QY 1596 GGAACAGTCTTTCTCAGAAATTTGTCAGGCTGGGAGGTCAACTTGTGTTCTTTCCCT 1655
Db 1021 GGAACAGTCTTTCTCAGAAATTTGTCAGGCTGGGAGGTCAACTTGTGTTCTTTCCCT 1080
QY 1656 CACCTGTGCTTCTTAAACGCTGCAAGTGTGTAGAGCAAAAGAGTGAAGTCA 1715
Db 1081 CACCTGTGCTTCTTAAACGCTGCAAGTGTGTAGAGCAAAAGAGTGAAGTCA 1140
QY 1716 GCACATCCGCTTCTGCCAGATGCTGGGGCCCGGCAACAGATTGAAGAGAGATCATG 1775
Db 1141 GCACATCCGCTTCTGCCAGATGCTGGGGCCCGGCAACAGATTGAAGAGAGATCATG 1200
QY 1776 TGAAGGGAGTGTGGTCAGGAGGCTCTCTGGTTTGGCCACTGGCCCTGATTTGAACCT 1835
Db 1201 TGAAGGGAGTGTGGTCAGGAGGCTCTCTGGTTTGGCCACTGGCCCTGATTTGAACCT 1260
QY 1836 GCCACTTGGAGAGCTCGGGGTGCTCCCTGGTTTCCCTCTCGAGAAATGAGCGGAGAG 1895
Db 1261 GCCACTTGGAGAGCTCGGGGTGCTCCCTGGTTTCCCTCTCGAGAAATGAGCGGAGAG 1320
QY 1896 GCCTCGCTTCTGAAGGAGCAGTGTGATGCCACTGGCTTAGTGTCTGGCTCACAGC 1955
Db 1321 GCCTCGCTTCTGAAGGAGCAGTGTGATGCCACTGGCTTAGTGTCTGGCTCACAGC 1380
QY 1956 TTCTTTGCAAGGCTGTCAAGGAAAGCAGCGGCTGGCACCTGAGCATATGCCCTCT 2015
Db 1381 TTCTTTGCAAGGCTGTCAAGGAAAGCAGCGGCTGGCACCTGAGCATATGCCCTCT 1440
QY 2016 TGGGGTCCCTCATCCAGCCGCTCGAGCTTTGACATCTTGTGTACTCATGTCTCTCT 2075
Db 1441 TGGGGTCCCTCATCCAGCCGCTCGAGCTTTGACATCTTGTGTACTCATGTCTCTCT 1500
QY 2076 CCTTGTGTACCCCTCCAGTATTACCATTTGCCCTCACCTGGCTTGGTGGGCTTT 2135
Db 1501 CCTTGTGTACCCCTCCAGTATTACCATTTGCCCTCACCTGGCTTGGTGGGCTTT 1560
QY 2136 TAGTGAAGACAGATGGGCTGTTTCCCCCACTCTGAGTGTGAGGTACATACAC 2195
Db 1561 TAGTGAAGACAGATGGGCTGTTTCCCCCACTCTGAGTGTGAGGTACATACAC 1620
QY 2196 AGCTCTTTTATTGCTCTTCTGCTCTGATGTTCTCTCTCTCTCTCTCTCTCTCTCT 2255
Db 1621 AGCTCTTTTATTGCTCTTCTGCTCTGATGTTCTCTCTCTCTCTCTCTCTCTCTCT 1680
QY 2256 AGCGAGGAGGGGTGCCCTCAGGGGCCGACACTAGTATGATGTCAGTGTCCAGTGAAC 2315

Db 1681 AGCGAGGAGGGGTG-CCTCAGGGGCCGACACTAGTATGATGTCAGTGTCCAGTGTGAAC 1739
QY 2316 AGCAGAAATTAACATGTTTGCACCAACCAAAAAAAAAAAAAAAAA 2356
Db 1740 AGCAGAAATTAACATGTTTGCACCAACCAAAAAAAAAAAAAAAAA 1780

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Job time : 1060 secs